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OM protein - protein search, using sw model

Run on: May 27, 2005, 08:27:23 ; Search time 161 Seconds
(without alignments)
1054.593 Million cell updates/sec

Title: US-10-734-510-7
Perfect score: 2325
Sequence: 1 MVSSAFAPSIILMSLSAL.....TYARENGQDFAKCGFVPE 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2325	100.0	439	2 AAW62858	AAW62858 Peniophor
2	2325	100.0	439	2 AAW74484	AAW74484 Peniophor
3	2325	100.0	439	2 AAY39895	AAY39895 P. lycii
4	2254	96.9	423	7 ADI66763	ADI66763 Peniophor
5	2248	96.7	423	7 ADI66783	ADI66783 Peniophor
6	2247	96.6	423	7 ADI66777	ADI66777 Peniophor
7	2246	96.6	423	7 ADI66835	ADI66835 Peniophor
8	2246	96.6	423	7 ADI66841	ADI66841 Peniophor
9	2246	96.6	423	7 ADI66837	ADI66837 Peniophor
10	2245	96.6	423	7 ADI66832	ADI66832 Peniophor
11	2245	96.6	423	7 ADI66845	ADI66845 Peniophor
12	2244	96.5	423	7 ADI66781	ADI66781 Peniophor
13	2244	96.5	423	7 ADI66778	ADI66778 Peniophor
14	2244	96.5	423	7 ADI66833	ADI66833 Peniophor
15	2243	96.5	423	7 ADI66843	ADI66843 Peniophor
16	2243	96.5	423	7 ADI66828	ADI66828 Peniophor
17	2242	96.4	423	7 ADI66836	ADI66836 Peniophor
18	2242	96.4	423	7 ADI66838	ADI66838 Peniophor
19	2241	96.4	423	7 ADI66782	ADI66782 Peniophor
20	2239	96.3	423	7 ADI66840	ADI66840 Peniophor
21	2238	96.3	419	3 AAY69573	AAY69573 Peniophor
22	2238	96.3	419	3 AAB20520	AAB20520 Peniophor
23	2238	96.3	419	8 ADL73086	ADL73086 Peniophor
24	2237	96.2	423	7 ADI66830	ADI66830 Peniophor
25	2237	96.2	423	7 ADI66822	ADI66822 Peniophor

26	2236	96.2	423	7 ADI66842	ADI66842 Peniophor
27	2235	96.1	423	7 ADI66839	ADI66839 Peniophor
28	2234	96.1	423	7 ADI66779	ADI66779 Peniophor
29	2233	96.0	423	7 ADI66844	ADI66844 Peniophor
30	2231	96.0	423	7 ADI66776	ADI66776 Peniophor
31	2231	96.0	423	7 ADI66829	ADI66829 Peniophor
32	2228	95.8	423	7 ADI66824	ADI66824 Peniophor
33	2227	95.8	423	7 ADI66780	ADI66780 Peniophor
34	2226	95.7	423	7 ADI66834	ADI66834 Peniophor
35	2225	95.7	423	7 ADI66825	ADI66825 Peniophor
36	2224	95.7	423	7 ADI66831	ADI66831 Peniophor
37	2223	95.6	423	7 ADI66820	ADI66820 Peniophor
38	2223	95.6	423	7 ADI66827	ADI66827 Peniophor
39	2222	95.6	423	7 ADI66823	ADI66823 Peniophor
40	2220	95.5	423	7 ADI66815	ADI66815 Peniophor
41	2219	95.4	423	7 ADI66819	ADI66819 Peniophor
42	2217	95.4	423	7 ADI66817	ADI66817 Peniophor
43	2216	95.3	423	7 ADI66821	ADI66821 Peniophor
44	2214	95.2	423	7 ADI66826	ADI66826 Peniophor
45	2212	95.1	423	7 ADI66818	ADI66818 Peniophor

ALIGNMENTS

RESULT 1
AAW62858
ID AAW62858 standard; protein; 439 AA.
XX
AC AAW62858;
XX
DT 17-OCT-2003 (revised)
DT 09-NOV-1998 (first entry)
XX
DE Peniophora lycii 6-phytase.
XX
KW 6-Phytase; basidiomycetes; feed additive; feedstuff.
XX
OS Peniophora lycii; strain CBS 686.96.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= Sig_peptide
FT 31..439
FT /label= Mat_protein
XX
PN WO9828409-A1.
XX
PD 02-JUL-1998.
XX
PF 15-DEC-1997; 97WO-DK000568.
XX
PR 20-DEC-1996; 96DK-00001480.
PR 20-DEC-1996; 96DK-00001481.
PR 18-MAR-1997; 97DK-00000301.
PR 07-MAY-1997; 97DK-00000529.
PR 01-DEC-1997; 97DK-00001388.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Lassen SF, Bech L, Ohmann A, Breinholt J, Fuglsang CC;
XX
DR WPI; 1998-377641/32.
XX
DR N-PSDB; AAV42331.
XX
PT Phytase(s) from fungi of phylum Basidiomycota - useful as feed and food
PT additives, e.g. to reduce phosphate content of manure and to improve
PT digestibility.
XX
PS Claim 25; Page 118-119; 197pp; English.
XX
CC This polypeptide comprises a 6-phytase of the basidiomycete Peniophora
CC lycii CBS 686.96. A cDNA clone (see AAW42331) encoding the enzyme was

CC obtained by expression cloning in yeast. The 6-phytase has been expressed
 CC in *Aspergillus oryzae*. The recombinant enzyme is very stable at 40 degC
 CC in the pH range 3-9, and 50-60% of activity is retained after 1 hr at 60-
 CC 80 degC; this may be due to the enzyme's ability to refold following
 CC thermal denaturation. The Peniophora phytase is more efficient than the
 CC known *Aspergillus* phytase in releasing inorganic phosphate from corn. It
 CC is essentially a 6-phytase, and at pH 3.5 is a phytase of hitherto
 CC unknown type, i.e. a 3+6-phytase. The invention provides basidiomycete
 CC phytases (see AAW62857-62), cloned DNA sequences (see AAV42330-35),
 CC processes for preparing the phytases, and their use especially as food or
 CC feed additives to improve digestibility. This novel subfamily of phytases
 CC have a high degree of conserved regions (see AAW62843-56) in common.
 CC Compared with known phytases, they show better heat stability or faster
 CC release of phosphate from substrates, and may also show advantageous
 CC position specificity and specific activity. They can be produced in
 CC commercially useful quantities. (Updated on 17-OCT-2003 to standardise OS
 CC field)

XX SQ Sequence 439 AA;

Query Match 100.0%; Score 2325; DB 2; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.4e-224;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVSSAFAPSIILLSSLSLSTQSFVAAQLPIPAQNTSNMGYPDPFFVPEYAAPPEGC 60
 DB 1 MVSSAFAPSIILLSSLSLSTQSFVAAQLPIPAQNTSNMGYPDPFFVPEYAAPPEGC 60
 QY 61 TTVQVNLIOHGGARWPTSGARSRQVAVAKIOMARPTDPKYEFLNDFYKFGVADLLPF 120
 DB 61 TTVQVNLIOHGGARWPTSGARSRQVAVAKIOMARPTDPKYEFLNDFYKFGVADLLPF 120
 QY 121 GANQSHQTGTDMYTRYSTLFEQGDVFPVRAAGDQVRVDSSTNWTAGFGDASGETVLTQ 180
 DB 121 GANQSHQTGTDMYTRYSTLFEQGDVFPVRAAGDQVRVDSSTNWTAGFGDASGETVLTQ 180
 QY 181 VVLQEGNCTLCNNMCPNEVDGDESTTTLGVPAPNITARLNAAAPSANLSDSALTMDM 240
 DB 181 VVLQEGNCTLCNNMCPNEVDGDESTTTLGVPAPNITARLNAAAPSANLSDSALTMDM 240
 QY 241 CPFDLTSSGNASPFCDLFTABEYVSVEYYDLDKYYGTGPGNALGPVQGVYNELLARL 300
 DB 241 CPFDLTSSGNASPFCDLFTABEYVSVEYYDLDKYYGTGPGNALGPVQGVYNELLARL 300
 QY 301 TQGAVRDETQTNRTLSDSDPATPLNRTFYADFSDNTWVPIFAALGLFNATALDPLKPE 360
 DB 301 TQGAVRDETQTNRTLSDSDPATPLNRTFYADFSDNTWVPIFAALGLFNATALDPLKPE 360
 QY 361 NRLWVDSKLVFPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQT 420
 DB 361 NRLWVDSKLVFPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQT 420
 QY 421 YARENGQGDFAKCGFVPS 439
 DB 421 YARENGQGDFAKCGFVPS 439

RESULT 2

AAW74484

ID AAW74484 standard; protein; 439 AA.

XX AC AAW74484;

XX DT 17-DEC-1998 (first entry)

XX DE Peniophora phytase polypeptide.

XX KW Phytase; inorganic phosphate; phytate; phytic acid.

XX OS Peniophora lycii.

XX PN WO9828408-A1.

XX XX

PD 02-JUL-1998.
 XX 10-DEC-1997; 97WO-DK000559.
 XX 20-DEC-1996; 96DK-00001481.
 PR 07-MAY-1997; 97DK-00000529.
 XX (NOVO) NOVO-NORDISK AS.
 XX Lassen SF, Bech L, Fuglsang CC, Breinholt J, Ohmann A;
 PI Ostergaard PR;
 XX WPI; 1998-467148/40.
 DR N-PSDB; AAV41837.
 XX New isolated Peniophora lycii phytase - used in human food or animal
 PT feed, for reducing phytate levels or improving protein availability or
 PT bio:availability of minerals.
 XX
 PS Claim 1; Page 54-57; 82pp; English.
 XX The present sequence represents a polypeptide exhibiting phytase activity
 CC encoded by a cDNA derived from Peniophora lycii. This protein has been
 CC found to have superior properties to known phytases such as increased
 CC heat stability or faster release of phytate. The polypeptide produced can
 CC be used in e.g. liberating inorganic phosphate from phytate or phytic
 CC acid, in human food or animal feed preparations or in additives for such
 CC preparations
 XX
 SQ Sequence 439 AA;
 Query Match 100.0%; Score 2325; DB 2; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.4e-224;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVSSAFAPSIILLSSLSLSTQSFVAAQLPIPAQNTSNMGYPDPFFVPEYAAPPEGC 60
 DB 1 MVSSAFAPSIILLSSLSLSTQSFVAAQLPIPAQNTSNMGYPDPFFVPEYAAPPEGC 60
 QY 61 TTVQVNLIOHGGARWPTSGARSRQVAVAKIOMARPTDPKYEFLNDFYKFGVADLLPF 120
 DB 61 TTVQVNLIOHGGARWPTSGARSRQVAVAKIOMARPTDPKYEFLNDFYKFGVADLLPF 120
 QY 121 GANQSHQTGTDMYTRYSTLFEQGDVFPVRAAGDQVRVDSSTNWTAGFGDASGETVLTQ 180
 DB 121 GANQSHQTGTDMYTRYSTLFEQGDVFPVRAAGDQVRVDSSTNWTAGFGDASGETVLTQ 180
 QY 181 VVLQEGNCTLCNNMCPNEVDGDESTTTLGVPAPNITARLNAAAPSANLSDSALTMDM 240
 DB 181 VVLQEGNCTLCNNMCPNEVDGDESTTTLGVPAPNITARLNAAAPSANLSDSALTMDM 240
 QY 241 CPFDLTSSGNASPFCDLFTABEYVSVEYYDLDKYYGTGPGNALGPVQGVYNELLARL 300
 DB 241 CPFDLTSSGNASPFCDLFTABEYVSVEYYDLDKYYGTGPGNALGPVQGVYNELLARL 300
 QY 301 TQGAVRDETQTNRTLSDSDPATPLNRTFYADFSDNTWVPIFAALGLFNATALDPLKPE 360
 DB 301 TQGAVRDETQTNRTLSDSDPATPLNRTFYADFSDNTWVPIFAALGLFNATALDPLKPE 360
 QY 361 NRLWVDSKLVFPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQT 420
 DB 361 NRLWVDSKLVFPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQT 420
 QY 421 YARENGQGDFAKCGFVPS 439
 DB 421 YARENGQGDFAKCGFVPS 439
 RESULT 3
 AAY39895
 ID AAY39895 standard; protein; 439 AA.
 XX AC AAY39895;
 AC

XX 27-AUG-2003 (revised)
 DT 07-DEC-1999 (first entry)
 DE P. lycii phytase protein sequence.
 XX Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
 KW phytate level reduction; animal manure; food preparation; soy processing;
 XX inositol manufacture.
 XX Peniophora lycii.
 OS WO9949022-A1.
 PN 30-SEP-1999.
 XX 22-MAR-1999; 99WO-DK000153.
 XX 23-MAR-1998; 98DK-00000407.
 PR 19-JUN-1998; 98DK-00000806.
 PR 18-SEP-1998; 98DK-00001176.
 PR 22-JAN-1999; 99DK-00000091.
 XX (NOVO) NOVO-NORDISK AS.
 PA Svendsen A;
 XX WPI; 1999-580444/49.
 DR N-PSDB; AA227412.
 XX New variant phytase enzymes, used for liberating phosphorus from a
 PT phytase substrate, for reducing phytate levels in animal manure and in
 PT feed and food preparations.
 XX Claim 1; Fig 6; 141pp; English.
 XX This sequence represents the Peniophora lycii phytase sequence. The
 CC invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate from
 CC corn, reaction rate, phytase degradation rate and end level of released
 CC phosphate reached. (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 439 AA;
 SQ
 Query Match 100.0%; Score 2325; DB 2; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.4e-224;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVSSAFAPSTLLSLSLSTQFSFVAAQLPIPAQNTSNWGPYDFPFVPEYAAPPEGC 60
 DB 1 MVSSAFAPSTLLSLSLSTQFSFVAAQLPIPAQNTSNWGPYDFPFVPEYAAPPEGC 60
 QY 61 TVTVQNLIQHGHARWPTSGARSQVAQVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
 DB 61 TVTVQNLIQHGHARWPTSGARSQVAQVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF 120
 QY 121 GANQSHQGTGDMTRYSTLTLEGGDVPFVRAAGQQRVVDSSNTWTAGDASGETVLTPLQ 180
 DB 121 GANQSHQGTGDMTRYSTLTLEGGDVPFVRAAGQQRVVDSSNTWTAGDASGETVLTPLQ 180
 QY 181 VVLQEGNCTLCNNMCPNEVDGDESTTTLGVFAPNITARLNAAAPSANLSDSALTMDM 240
 DB 181 VVLQEGNCTLCNNMCPNEVDGDESTTTLGVFAPNITARLNAAAPSANLSDSALTMDM 240

QY 241 CPFDTLSSGNASPFCDLFTAEYVSVEYYDLDKYTGCGNALGPGVQGVYNELLARL 300
 DB 241 CPFDTLSSGNASPFCDLFTAEYVSVEYYDLDKYTGCGNALGPGVQGVYNELLARL 300
 QY 301 TQGAVRDEQTQNRTLSDSDPATPPLNRTFYADFSHDNTWPIPAALGLFNATLDPKPDPE 360
 DB 301 TQGAVRDEQTQNRTLSDSDPATPPLNRTFYADFSHDNTWPIPAALGLFNATLDPKPDPE 360
 QY 361 NRLWVDSKLVFPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGCGVDGVCLSAFVESQT 420
 DB 361 NRLWVDSKLVFPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGCGVDGVCLSAFVESQT 420
 QY 421 YARENGQGDFAKCGFVPE 439
 DB 421 YARENGQGDFAKCGFVPE 439
 RESULT 4
 ADI66763
 ID ADI66763 standard; protein; 423 AA.
 XX AC ADI66763;
 XX DT 22-APR-2004 (first entry)
 XX Peniophora lycii phytase SEQ ID NO:2.
 DE phytase; nutritional value; growth rate; weight gain; feed conversion.
 KW Peniophora lycii.
 OS WO2003066847-A2.
 XX 14-AUG-2003.
 XX 04-FEB-2003; 2003WO-DK000067.
 XX 08-FEB-2002; 2002DK-00000193.
 XX 30-SEP-2002; 2002DK-00001449.
 XX (NOVO) NOVOZYMES AS.
 PA Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
 WPI; 2003-663595/62.
 DR N-PSDB; ADI66762.
 XX New phytase variants useful as animal feed additives and for treating
 PT plant material and manure.
 XX Claim 1; SEQ ID NO 2; 124pp; English.
 XX The invention relates to novel active phytase variants (I) with one or
 CC more specific substitutions. The phytase variants of the invention are
 CC useful for improving the nutritional value of animal feed compositions
 CC (e.g. to increase growth rate, weight gain and/or feed conversion),
 CC reducing phytate levels in animal manure, treating vegetables or
 CC proteins, and liberating phosphorus from a phytase substrate. The
 CC present sequence represents the phytase used in the invention.
 XX Sequence 423 AA;
 SQ
 Query Match 96.9%; Score 2254; DB 7; Length 423;
 Best Local Similarity 100.0%; Pred. No. 1.8e-217;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 SLALSTQFSFVAAQLPIPAQNTSNWGPYDFPFVPEYAAPPEGCTTVQNLIQHGHARWP 76
 DB 1 SLALSTQFSFVAAQLPIPAQNTSNWGPYDFPFVPEYAAPPEGCTTVQNLIQHGHARWP 60
 QY 77 TSGARSQVAQVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPFGANQSHQGTGDMTRY 136

Db 61 TSGARSRQVAQVAKIQMARPFDDPKYEFNLDFVYKFGVADLLPFGANQSHQGTDMYTRY 120
QY 137 STLFEFGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPVLQVVLQBEQGNCTLCNNMC 196
Db 121 STLFEFGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPVLQVVLQBEQGNCTLCNNMC 180
QY 197 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDCPFDLTSSGNASPPCD 256
Db 181 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDCPFDLTSSGNASPPCD 240
QY 257 LFTAEEYVSYYEYDLDKYGTGPGNALGPVQGVVNNELLARLTGQAVRDETQTNRTILD 316
Db 241 LFTAEEYVSYYEYDLDKYGTGPGNALGPVQGVVNNELLARLTGQAVRDETQTNRTILD 300
QY 317 SDPATFPLNRTFYADFSHDNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHM 376
Db 301 SDPATFPLNRTFYADFSHDNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHM 360
QY 377 TVEKLACSGKEAVRVLVNDVQVPLEFCGCGVDGVCLSAFVESQTYARENGQGDFAKCGFV 436
Db 361 TVEKLACSGKEAVRVLVNDVQVPLEFCGCGVDGVCLSAFVESQTYARENGQGDFAKCGFV 420
QY 437 PSE 439
Db 421 PSE 423
RESULT 5
ADI66783
ID ADI66783 standard; protein; 423 AA.
AC ADI66783;
XX
XX
DT 22-APR-2004 (first entry)
DE Peniophora lycii phytase mutant (viii).
XX phytase; nutritional value; growth rate; weight gain; feed conversion;
KW mutant; mutein.
XX
OS Peniophora lycii.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 29 /label= Wild-type D substituted by S
XX WO2003066847-A2.
XX
XX 14-AUG-2003.
XX
XX 04-FEB-2003; 2003WO-DK000067.
XX
XX 08-FEB-2002; 2002DK-00000193.
PR 30-SEP-2002; 2002DK-00001449.
XX
XX (NOVO) NOVOZYMES AS.
XX
XX Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX WPI; 2003-663595/62.
XX
XX New phytase variants useful as animal feed additives and for treating
FT plant material and manure.
XX
XX Claim 2; Page; 124pp; English.
XX
XX The invention relates to novel active phytase variants (I) with one or
CC more specific substitutions. The phytase variants of the invention are
CC useful for improving the nutritional value of animal feed compositions
CC (e.g. to increase growth rate, weight gain and/or feed conversion),
CC reducing phytate levels in animal manure, treating vegetables or
CC proteins, and liberating phosphorous from a phytase substrate. The

CC present sequence represents a variant phytase of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ Sequence 423 AA;
Query Match 96.7%; Score 2248; DB 7; Length 423;
Best Local Similarity 99.8%; Pred. No. 7.4e-217;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 17 SLALSTQFSFVAAQLPPIPAQNTSNNGPVDPPFPVPEYAAPPGCTVTVNLLQRHGARP 76
Db 1 SLALSTQFSFVAAQLPPIPAQNTSNNGPYSPPFPVPEYAAPPGCTVTVNLLQRHGARP 60
QY 77 TSGARSRQVAQVAKIQMARPFDDPKYEFNLDFVYKFGVADLLPFGANQSHQGTDMYTRY 136
Db 61 TSGARSRQVAQVAKIQMARPFDDPKYEFNLDFVYKFGVADLLPFGANQSHQGTDMYTRY 120
QY 137 STLFEFGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPVLQVVLQBEQGNCTLCNNMC 196
Db 121 STLFEFGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPVLQVVLQBEQGNCTLCNNMC 180
QY 197 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDCPFDLTSSGNASPPCD 256
Db 181 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMDCPFDLTSSGNASPPCD 240
QY 257 LFTAEEYVSYYEYDLDKYGTGPGNALGPVQGVVNNELLARLTGQAVRDETQTNRTILD 316
Db 241 LFTAEEYVSYYEYDLDKYGTGPGNALGPVQGVVNNELLARLTGQAVRDETQTNRTILD 300
QY 317 SDPATFPLNRTFYADFSHDNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHM 376
Db 301 SDPATFPLNRTFYADFSHDNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHM 360
QY 377 TVEKLACSGKEAVRVLVNDVQVPLEFCGCGVDGVCLSAFVESQTYARENGQGDFAKCGFV 436
Db 361 TVEKLACSGKEAVRVLVNDVQVPLEFCGCGVDGVCLSAFVESQTYARENGQGDFAKCGFV 420
QY 437 PSE 439
Db 421 PSE 423
RESULT 6
ADI66777
ID ADI66777 standard; protein; 423 AA.
XX
XX ADI66777;
XX
XX 22-APR-2004 (first entry)
XX
XX Peniophora lycii phytase mutant (ii).
DE phytase; nutritional value; growth rate; weight gain; feed conversion;
KW mutant; mutein.
XX
OS Peniophora lycii.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 29 /label= Wild-type D substituted by N
FT Misc-difference 102 /note= "Wild-type L substituted by I"
XX
XX WO2003066847-A2.
XX
XX 14-AUG-2003.
XX
XX 04-FEB-2003; 2003WO-DK000067.
XX
XX 08-FEB-2002; 2002DK-00000193.
PR 30-SEP-2002; 2002DK-00001449.

XX PA (NOVO) NOVOZYMES AS.
 XX PI Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
 XX DR WPI; 2003-663595/62.
 XX FT New phytase variants useful as animal feed additives and for treating
 PT plant material and manure.
 XX PS Claim 2; Page; 124pp; English.
 XX CC The invention relates to novel active phytase variants (I) with one or
 CC more specific substitutions. The phytase variants of the invention are
 CC useful for improving the nutritional value of animal feed compositions
 CC (e.g. to increase growth rate, weight gain and/or feed conversion),
 CC reducing phytate levels in animal manure, treating vegetables or
 CC proteins, and liberating phosphorous from a phytase substrate. The
 CC present sequence represents a variant phytase of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from
 CC the Peniophora lycii phytase sequence shown in ADI66763.
 XX SQ Sequence 423 AA;

Query Match 96.6%; Score 2247; DB 7; Length 423;
 Best Local Similarity 99.5%; Pred. No. 9.3e-217; Indels 0; Gaps 0;
 Matches 421; Conservative 2; Mismatches 0;

QY 17 SLALSTQFSFVAALPIPAQNTSNMGPDYDFFVPEYAAPPEGCTVTQVNLQIQRHGARP 76
 DB 1 SLALSTQFSFVAALPIPAQNTSNMGPDYDFFVPEYAAPPEGCTVTQVNLQIQRHGARP 60
 QY 77 TSGARSRQVAAVAKIQMARPFDDPKYEFNLDFVYKFGVADLLPFGANQSHQGTDMYTRY 136
 DB 61 TSGARSRQVAAVAKIQMARPFDDPKYEFNLDFVYKFGVADLLPFGANQSHQGTDMYTRY 120
 QY 137 STLFEFGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLP TLQVVLQEGNCTLCNNMC 196
 DB 121 STLFEFGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLP TLQVVLQEGNCTLCNNMC 180
 QY 197 PNEVDGESTTWLGVFAPNITARLNAAPSANLSDSALTMDMCPFDTLSSGNASPFCD 256
 DB 181 PNEVDGESTTWLGVFAPNITARLNAAPSANLSDSALTMDMCPFDTLSSGNASPFCD 240
 QY 257 LFTABEYVSYYEYDLDKYYGTGPGNALGPVQGVGVYNELLARLTQAVRDETQTNR TLD 316
 DB 241 LFTABEYVSYYEYDLDKYYGTGPGNALGPVQGVGVYNELLARLTQAVRDETQTNR TLD 300
 QY 317 SDPATPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPSGHM 376
 DB 301 SDPATPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPSGHM 360
 QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQTYARENGQGFV 436
 DB 361 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQTYARENGQGFV 420
 QY 437 PSE 439
 DB 421 PSE 423

- RESULT 7
 ADI66835
 ID ADI66835 standard; protein; 423 AA.
 XX AC ADI66835;
 XX DT 22-APR-2004 (first entry)
 XX DE Peniophora lycii phytase mutant (1x).
 XX KW phytase; nutritional value; growth rate; weight gain; feed conversion;
 KW mutant; mutein.

XX Peniophora lycii.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 218 /label= Wild-type A substituted by T
 FT Misc-difference 334 /note= "Wild-type A substituted by G"
 FT
 XX WO2003066847-A2.
 XX PN 14-AUG-2003.
 XX PD 04-FEB-2003; 2003WO-DK0000067.
 XX PF 08-FEB-2002; 2002DK-00000193.
 XX PR 30-SEP-2002; 2002DK-00001449.
 XX PA (NOVO) NOVOZYMES AS.
 XX PI Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
 XX DR WPI; 2003-663595/62.
 XX FT New phytase variants useful as animal feed additives and for treating
 PT plant material and manure.
 XX PS Claim 2; Page; 124pp; English.
 XX CC The invention relates to novel active phytase variants (I) with one or
 CC more specific substitutions. The phytase variants of the invention are
 CC useful for improving the nutritional value of animal feed compositions
 CC (e.g. to increase growth rate, weight gain and/or feed conversion),
 CC reducing phytate levels in animal manure, treating vegetables or
 CC proteins, and liberating phosphorous from a phytase substrate. The
 CC present sequence represents a variant phytase of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from
 CC the Peniophora lycii phytase sequence shown in ADI66763.
 XX SQ Sequence 423 AA;

Query Match 96.6%; Score 2246; DB 7; Length 423;
 Best Local Similarity 99.5%; Pred. No. 1.2e-216; Indels 0; Gaps 0;
 Matches 421; Conservative 0; Mismatches 2;

QY 17 SLALSTQFSFVAALPIPAQNTSNMGPDYDFFVPEYAAPPEGCTVTQVNLQIQRHGARP 76
 DB 1 SLALSTQFSFVAALPIPAQNTSNMGPDYDFFVPEYAAPPEGCTVTQVNLQIQRHGARP 60
 QY 77 TSGARSRQVAAVAKIQMARPFDDPKYEFNLDFVYKFGVADLLPFGANQSHQGTDMYTRY 136
 DB 61 TSGARSRQVAAVAKIQMARPFDDPKYEFNLDFVYKFGVADLLPFGANQSHQGTDMYTRY 120
 QY 137 STLFEFGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLP TLQVVLQEGNCTLCNNMC 196
 DB 121 STLFEFGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLP TLQVVLQEGNCTLCNNMC 180
 QY 197 PNEVDGESTTWLGVFAPNITARLNAAPSANLSDSALTMDMCPFDTLSSGNASPFCD 256
 DB 181 PNEVDGESTTWLGVFAPNITARLNAAPSANLSDSALTMDMCPFDTLSSGNASPFCD 240
 QY 257 LFTABEYVSYYEYDLDKYYGTGPGNALGPVQGVGVYNELLARLTQAVRDETQTNR TLD 316
 DB 241 LFTABEYVSYYEYDLDKYYGTGPGNALGPVQGVGVYNELLARLTQAVRDETQTNR TLD 300
 QY 317 SDPATPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPSGHM 376
 DB 301 SDPATPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPSGHM 360
 QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQTYARENGQGFV 436
 DB 361 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQTYARENGQGFV 420

QY 437 PSE 439
DB 421 PSE 423

RESULT 8
ADI66841
ADI66841 standard; protein; 423 AA.

XX
AC ADI66841;
XX
DT 22-APR-2004 (first entry)
XX
DE Peniophora lycii phytase mutant (lxvi).
XX
KW phytase; nutritional value; growth rate; weight gain; feed conversion;
KW mutant; mutein.
XX
OS Peniophora lycii.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 330 /label= Wild-type R substituted by R
XX
XX WO2003066847-A2.
XX
XX 14-AUG-2003.
XX
XX 04-FEB-2003; 2003WO-DK000067.
XX
XX 08-FEB-2002; 2002DK-00000193.
XX
XX 30-SEP-2002; 2002DK-00001449.
XX
XX (NOVO) NOVOZYMES AS.
XX
XX Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX WPI; 2003-663595/62.
XX
XX New phytase variants useful as animal feed additives and for treating
XX plant material and manure.
XX
XX Claim 2; Page; 124pp; English.
XX
XX The invention relates to novel active phytase variants (I) with one or
XX more specific substitutions. The phytase variants of the invention are
XX useful for improving the nutritional value of animal feed compositions
XX (e.g. to increase growth rate, weight gain and/or feed conversion),
XX reducing phytate levels in animal manure, treating vegetables or
XX proteins, and liberating phosphorous from a phytase substrate. The
XX present sequence represents a variant phytase of the invention. Note: The
XX present sequence is not shown in the specification but is derived from
XX the Peniophora lycii phytase sequence shown in ADI66763.

XX
SQ Sequence 423 AA;

Query Match 96.6%; Score 2246; DB 7; Length 423;
Best Local Similarity 99.8%; Pred. No. 1.2e-216;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 SLALSTQFSFVAQLPIPAQNTSNMGYPDPFFPVEPYAAPPGCTTQVNLQIRHGARP 76
DB 1 SLALSTQFSFVAQLPIPAQNTSNMGYPDPFFPVEPYAAPPGCTTQVNLQIRHGARP 60
QY 77 TSGARSQVAAVAKIQMARPPDTPKTEFLNDFYKFGVADLLPFGANQSHQTGDMYTRY 136
DB 61 TSGARSQVAAVAKIQMARPPDTPKTEFLNDFYKFGVADLLPFGANQSHQTGDMYTRY 120
QY 137 STLFEQGDVPFRAAGDQRVDSSTNWTAGFDASGETVLPLOVVLQEEGNTLCNNMC 196
DB 121 STLFEQGDVPFRAAGDQRVDSSTNWTAGFDASGETVLPLOVVLQEEGNTLCNNMC 180

QY 197 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMCMCPFDLTSSGNASPFCD 256
DB 181 PNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSDALTLMCMCPFDLTSSGNASPFCD 240
QY 257 LFTABEYVSYYEYDLDKYYGTGPGNALGPVQGVYVNEELLARLTQOAVRDETQTNRTLD 316
DB 241 LFTABEYVSYYEYDLDKYYGTGPGNALGPVQGVYVNEELLARLTQOAVRDETQTNRTLD 300
QY 317 SDPATPPLNRTFYADPFSHDNTMVP;FAALGLFNATALDPLKPDENRLWVDSKLVPSGHHM 376
DB 301 SDPATPPLNRTFYADPFSHDNTMVP;FAALRLFNATALDPLKPDENRLWVDSKLVPSGHHM 360
QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVGVDCVCELSAFVESQTYARENGQGDFAKCGFV 436
DB 361 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVGVDCVCELSAFVESQTYARENGQGDFAKCGFV 420
QY 437 PSE 439
DB 421 PSE 423

RESULT 9
ADI66837
ID ADI66837 standard; protein; 423 AA.
XX
AC ADI66837;
XX
XX 22-APR-2004 (first entry)
XX
DE Peniophora lycii phytase mutant (lxii).
XX
KW phytase; nutritional value; growth rate; weight gain; feed conversion;
KW mutant; mutein.
XX
OS Peniophora lycii.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Misc-difference 324 /label= Wild-type P substituted by S
XX
XX WO2003066847-A2.
XX
XX 14-AUG-2003.
XX
XX 04-FEB-2003; 2003WO-DK000067.
XX
XX 08-FEB-2002; 2002DK-00000193.
XX
XX 30-SEP-2002; 2002DK-00001449.
XX
XX (NOVO) NOVOZYMES AS.
XX
XX Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX WPI; 2003-663595/62.
XX
XX New phytase variants useful as animal feed additives and for treating
XX plant material and manure.
XX
XX Claim 2; Page; 124pp; English.
XX
XX The invention relates to novel active phytase variants (I) with one or
XX more specific substitutions. The phytase variants of the invention are
XX useful for improving the nutritional value of animal feed compositions
XX (e.g. to increase growth rate, weight gain and/or feed conversion),
XX reducing phytate levels in animal manure, treating vegetables or
XX proteins, and liberating phosphorous from a phytase substrate. The
XX present sequence represents a variant phytase of the invention. Note: The
XX present sequence is not shown in the specification but is derived from
XX the Peniophora lycii phytase sequence shown in ADI66763.

XX
SQ Sequence 423 AA;

Query Match 96.6%; Score 2246; DB 7; Length 423;
Best Local Similarity 99.8%; Pred. No. 1.2e-216;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 SLALSTQFSFVAQAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGCTVTQVNLQIQRHGARP 76
DB 1 SLALSTQFSFVAQAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGCTVTQVNLQIQRHGARP 60

QY 77 TSGARSRQAAVAKIQMARPFDDPKYEFVNDVYKFGVADLLPFGANQSHQGTDMYTRY 136
DB 61 TSGARSRQAAVAKIQMARPFDDPKYEFVNDVYKFGVADLLPFGANQSHQGTDMYTRY 120

QY 137 STLFEQGDVFPVRAAGDQRVVDSTNTWTAGFSDASGETVLPVQLVQVLEBEGNCTLCNNMC 196
DB 121 STLFEQGDVFPVRAAGDQRVVDSTNTWTAGFSDASGETVLPVQLVQVLEBEGNCTLCNNMC 180

QY 197 PNEVDGDESTTWLGVPAPNITARLNAAAPSANLSDSALTMDMCPFDLTSSGNASPFCD 256
DB 181 PNEVDGDESTTWLGVPAPNITARLNAAAPSANLSDSALTMDMCPFDLTSSGNASPFCD 240

QY 257 LFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVYVNNELLARLTGQAVRDETQTNRTLD 316
DB 241 LFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVYVNNELLARLTGQAVRDETQTNRTLD 300

QY 317 SDPATFPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
DB 301 SDPATFPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 360

QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
DB 361 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 420

QY 437 PSE 439
DB 421 PSE 423

RESULT 10:
ADI66832
ID ADI66832 standard; protein; 423 AA.
AC ADI66832;
XX
XX 22-APR-2004 (first entry)
XX Peniophora lycii phytase mutant (lvii).
XX phytase; nutritional value; growth rate; weight gain; feed conversion;
XX mutant; mutein.
XX Peniophora lycii.
XX Synthetic.
XX Key Location/Qualifiers

FT Misc-difference 69
FT FT /label= Wild-type V substituted by A
FT FT /label= Wild-type V substituted by A
FT FT /note= "Wild-type A substituted by E"
XX
XX WQ2003066847-A2.
XX
XX 14-AUG-2003.
XX
XX 04-FEB-2003; 2003WO-DK000067.
XX
XX 08-FEB-2002; 2002DK-00000193.
XX 30-SEP-2002; 2002DK-00001449.
XX
XX (NOVO) NOVOZYMES AS.
XX
XX Matsui T, Fugisang CC, Svendsen A, Fukuyama S;
XX

DR WPI; 2003-663595/62.
XX New phytase variants useful as animal feed additives and for treating
PT plant material and manure.
XX
XX Claim 2; Page; 124pp; English.
XX
XX The invention relates to novel active phytase variants (I) with one or
CC more specific substitutions. The phytase variants of the invention are
CC useful for improving the nutritional value of animal feed compositions
CC (e.g. to increase growth rate, weight gain and/or feed conversion),
CC reducing phytase levels in animal manure, treating vegetables or
CC proteins, and liberating phosphorous from a phytase substrate. The
CC present sequence represents a variant phytase of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ Sequence 423 AA;

Query Match 96.6%; Score 2245; DB 7; Length 423;
Best Local Similarity 99.5%; Pred. No. 1.5e-216;
Matches 421; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 SLALSTQFSFVAQAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGCTVTQVNLQIQRHGARP 76
DB 1 SLALSTQFSFVAQAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGCTVTQVNLQIQRHGARP 60

QY 77 TSGARSRQAAVAKIQMARPFDDPKYEFVNDVYKFGVADLLPFGANQSHQGTDMYTRY 136
DB 61 TSGARSRQAAVAKIQMARPFDDPKYEFVNDVYKFGVADLLPFGANQSHQGTDMYTRY 120

QY 137 STLFEQGDVFPVRAAGDQRVVDSTNTWTAGFSDASGETVLPVQLVQVLEBEGNCTLCNNMC 196
DB 121 STLFEQGDVFPVRAAGDQRVVDSTNTWTAGFSDASGETVLPVQLVQVLEBEGNCTLCNNMC 180

QY 197 PNEVDGDESTTWLGVPAPNITARLNAAAPSANLSDSALTMDMCPFDLTSSGNASPFCD 256
DB 181 PNEVDGDESTTWLGVPAPNITARLNAAAPSANLSDSALTMDMCPFDLTSSGNASPFCD 240

QY 257 LFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVYVNNELLARLTGQAVRDETQTNRTLD 316
DB 241 LFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVYVNNELLARLTGQAVRDETQTNRTLD 300

QY 317 SDPATFPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 376
DB 301 SDPATFPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPFSGHM 360

QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 436
DB 361 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCELSAFVESQTYARENGQGDFAKCGFV 420

QY 437 PSE 439
DB 421 PSE 423

RESULT 11:
ADI66845
ID ADI66845 standard; protein; 423 AA.
XX
XX AC ADI66845;
XX
XX 22-APR-2004 (first entry)
XX Peniophora lycii phytase mutant (lvii).
XX phytase; nutritional value; growth rate; weight gain; feed conversion;
XX mutant; mutein.
XX Peniophora lycii.
XX Synthetic.
XX Key Location/Qualifiers


```
QY 257 LFTABEYVSVEYYDLDKYYGTGPGNALGPVQGVYVNNELLARLTGOAVRDETQTNRTLD 316
Db 241 LFTABEYVSVEYYDLDKYYGTGPGNALGPVQGVYVNNELLARLTGOAVRDETQTNRTLD 300
QY 317 SDPATPPLNRTFYADFSDHNTMVPPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHM 376
Db 301 SDPATPPLNRTFYADFSDHNTMVPPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHM 360
QY 377 TVEKLACSGKEAVRVLVNDVQVLEPCGGVDGVCSELSAFVESQTYARENGQGFACKGFV 436
Db 361 TVEKLACSGKEAVRVLVNDVQVLEPCGGVDGVCSELSAFVESQTYARENGQGFACKGFV 420
QY 437 PSE 439
Db 421 PSE 423

RESULT 13
ADI66778
ID ADI66778 standard; protein; 423 AA.
XX
AC ADI66778;
XX
DT 22-APR-2004 (first entry)
XX
DE Peniophora lycii phytase mutant (iii).
XX
KW phytase; nutritional value; growth rate; weight gain; feed conversion;
KW mutant; mutein.
XX
OS Peniophora lycii.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 29 /label= Wild-type D substituted by N
FT Misc-difference 118 /note= "Wild-type T substituted by A"
FT
XX
PN WO2003066847-A2.
XX
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003WO-DK000067.
XX
PR 08-FEB-2002; 2002DK-00000193.
XX
PR 30-SEP-2002; 2002DK-00001449.
XX
PA (NOVO ) NOVOZYMES AS.
XX
PI Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR WPI; 2003-663595/62.
XX
PT New phytase variants useful as animal feed additives and for treating
PT plant material and manure.
XX
PS Claim 2; Page; 124pp; English.
XX
CC The invention relates to novel active phytase variants (I) with one or
CC more specific substitutions. The phytase variants of the invention are
CC useful for improving the nutritional value of animal feed compositions
CC (e.g. to increase growth rate, weight gain and/or feed conversion),
CC reducing phytate levels in animal manure, treating vegetables or
CC proteins, and liberating phosphorous from a phytase substrate. The
CC present sequence represents a variant phytase of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ Sequence 423 AA;

Query Match 96.5%; Score 2244; DB 7; Length 423;
Best Local Similarity 99.5%; Pred. No. 1.9e-216;
```

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Matches 421; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 17 SLALSTQFSFVAAQLPIPAQNTSNMGPDYPPFPVEPYAAPPEGCTVTQNLIQRHGARWP 76
Db 1 SLALSTQFSFVAAQLPIPAQNTSNMGPDYPPFPVEPYAAPPEGCTVTQNLIQRHGARWP 60
QY 77 TSGARSQVAAVAKIQMARPFDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 136
Db 61 TSGARSQVAAVAKIQMARPFDPKYEFLNDFVYKFGVADLLPFGANQSHQTGTDMYTRY 120
QY 137 STLFEQGDVPPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPTLQVVLQEGNCTLCNNMC 196
Db 121 STLFEQGDVPPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPTLQVVLQEGNCTLCNNMC 180
QY 197 PNEVDGESTTWLGVFAPNITARLNAAPSANLSQSDALTMDMCPFDLTSSGNA3PFCD 256
Db 181 PNEVDGESTTWLGVFAPNITARLNAAPSANLSQSDALTMDMCPFDLTSSGNA3PFCD 240
QY 257 LFTABEYVSVEYYDLDKYYGTGPGNALGPVQGVYVNNELLARLTGOAVRDETQTNRTLD 316
Db 241 LFTABEYVSVEYYDLDKYYGTGPGNALGPVQGVYVNNELLARLTGOAVRDETQTNRTLD 300
QY 317 SDPATPPLNRTFYADFSDHNTMVPPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHM 376
Db 301 SDPATPPLNRTFYADFSDHNTMVPPIFAALGLFNATALDPLKPDENRLWVDSKLVPPSGHM 360
QY 377 TVEKLACSGKEAVRVLVNDVQVLEPCGGVDGVCSELSAFVESQTYARENGQGFACKGFV 436
Db 361 TVEKLACSGKEAVRVLVNDVQVLEPCGGVDGVCSELSAFVESQTYARENGQGFACKGFV 420
QY 437 PSE 439
Db 421 PSE 423

RESULT 14
ADI66833
ID ADI66833 standard; protein; 423 AA.
XX
AC ADI66833;
XX
DT 22-APR-2004 (first entry)
XX
DE Peniophora lycii phytase mutant (lviii).
XX
KW phytase; nutritional value; growth rate; weight gain; feed conversion;
KW mutant; mutein.
XX
OS Peniophora lycii.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 99 /label= Wild-type A substituted by D
FT Misc-difference 398 /note= "Wild-type A substituted by T"
FT
XX
PN WO2003066847-A2.
XX
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003WO-DK000067.
XX
PR 08-FEB-2002; 2002DK-00000193.
XX
PR 30-SEP-2002; 2002DK-00001449.
XX
PA (NOVO ) NOVOZYMES AS.
XX
PI Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX
DR WPI; 2003-663595/62.
XX
PT New phytase variants useful as animal feed additives and for treating
```

```
PT plant material and manure.
XX Claim 2; Page; 124pp; English.
XX
CC The invention relates to novel active phytase variants (I) with one or
CC more specific substitutions. The phytase variants of the invention are
CC useful for improving the nutritional value of animal feed compositions
CC (e.g. to increase growth rate, weight gain and/or feed conversion),
CC reducing phytate levels in animal manure, treating vegetables or
CC proteins, and liberating phosphorous from a phytase substrate. The
CC present sequence represents a variant phytase of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ Sequence 423 AA;

Query Match          96.5%; Score 2244; DB 7; Length 423;
Best Local Similarity 99.5%; Pred. No. 1.9e-216;
Matches 421; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFVPEFYAAPPEGCTVTQVNLQRHGAWP 76
   |||||||
Db 1 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFVPEFYAAPPEGCTVTQVNLQRHGAWP 60

QY 77 TSGARSRQVAAVAKIQMARPTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGDMYTRY 136
   |||||||
Db 61 TSGARSRQVAAVAKIQMARPTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGDMYTRY 120

QY 137 STLFEGGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPLOVVLQEGNCTLCNNMC 196
   |||||||
Db 121 STLFEGGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPLOVVLQEGNCTLCNNMC 180

QY 197 PNEVDGDESTTWLGVFAPNITARLNAAPSANLSDSDALTLMDCPFDTLSSGNASPFCD 256
   |||||||
Db 181 PNEVDGDESTTWLGVFAPNITARLNAAPSANLSDSDALTLMDCPFDTLSSGNASPFCD 240

QY 257 LFTAEEYVSYYEYDLDKYYGTGPGNALGPVQGVGVNELLARLTQAVRDETQTNRTILD 316
   |||||||
Db 241 LFTAEEYVSYYEYDLDKYYGTGPGNALGPVQGVGVNELLARLTQAVRDETQTNRTILD 300

QY 317 SDPATFPLNRTFYADFSHDNTMWPIFAALGLFNATALDPLKPDENRLWVDSKLVPSFGHM 376
   |||||||
Db 301 SDPATFPLNRTFYADFSHDNTMWPIFAALGLFNATALDPLKPDENRLWVDSKLVPSFGHM 360

QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCSELSAFVESQTYARENGQGDFAKCGFV 436
   |||||||
Db 361 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCSELSAFVESQTYARENGQGDFAKCGFV 420

QY 437 PSE 439
   |||
Db 421 PSE 423

RESULT 15
ADI66843
ID ADI66843 standard; protein; 423 AA.
XX
AC ADI66843;
XX
DT 22-APR-2004 (first entry)
XX
DE Peniophora lycii phytase mutant (lxviii).
XX
KW phytase; nutritional value; growth rate; weight gain; feed conversion;
KM mutant; mutein.
XX
OS Peniophora lycii.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 334
FT Misc-difference 344
FT Misc-difference 344
```

```
FT plant material and manure.
XX Claim 2; Page; 124pp; English.
XX
PD 14-AUG-2003.
XX
XX 04-FEB-2003; 2003WO-DK000067.
XX 08-FEB-2002; 2002DK-00000193.
XX 30-SEP-2002; 2002DK-00001449.
XX (NOVO ) NOVOZYMES AS.
XX
PI Matsui T, Fuglsang CC, Svendsen A, Fukuyama S;
XX WPI; 2003-663595/62.
XX
XX New phytase variants useful as animal feed additives and for treating
XX plant material and manure.
XX
PS Claim 2; Page; 124pp; English.
XX
CC The invention relates to novel active phytase variants (I) with one or
CC more specific substitutions. The phytase variants of the invention are
CC useful for improving the nutritional value of animal feed compositions
CC (e.g. to increase growth rate, weight gain and/or feed conversion),
CC reducing phytate levels in animal manure, treating vegetables or
CC proteins, and liberating phosphorous from a phytase substrate. The
CC present sequence represents a variant phytase of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the Peniophora lycii phytase sequence shown in ADI66763.
XX
SQ Sequence 423 AA;

Query Match          96.5%; Score 2243; DB 7; Length 423;
Best Local Similarity 99.5%; Pred. No. 2.3e-216;
Matches 421; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFVPEFYAAPPEGCTVTQVNLQRHGAWP 76
   |||||||
Db 1 SLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFVPEFYAAPPEGCTVTQVNLQRHGAWP 60

QY 77 TSGARSRQVAAVAKIQMARPTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGDMYTRY 136
   |||||||
Db 61 TSGARSRQVAAVAKIQMARPTDPKYEFLNDFVYKFGVADLLPFGANQSHQTGDMYTRY 120

QY 137 STLFEGGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPLOVVLQEGNCTLCNNMC 196
   |||||||
Db 121 STLFEGGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPLOVVLQEGNCTLCNNMC 180

QY 197 PNEVDGDESTTWLGVFAPNITARLNAAPSANLSDSDALTLMDCPFDTLSSGNASPFCD 256
   |||||||
Db 181 PNEVDGDESTTWLGVFAPNITARLNAAPSANLSDSDALTLMDCPFDTLSSGNASPFCD 240

QY 257 LFTAEEYVSYYEYDLDKYYGTGPGNALGPVQGVGVNELLARLTQAVRDETQTNRTILD 316
   |||||||
Db 241 LFTAEEYVSYYEYDLDKYYGTGPGNALGPVQGVGVNELLARLTQAVRDETQTNRTILD 300

QY 317 SDPATFPLNRTFYADFSHDNTMWPIFAALGLFNATALDPLKPDENRLWVDSKLVPSFGHM 376
   |||||||
Db 301 SDPATFPLNRTFYADFSHDNTMWPIFAALGLFNATALDPLKPDENRLWVDSKLVPSFGHM 360

QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCSELSAFVESQTYARENGQGDFAKCGFV 436
   |||||||
Db 361 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCSELSAFVESQTYARENGQGDFAKCGFV 420

QY 437 PSE 439
   |||
Db 421 PSE 423

Search completed: May 27, 2005, 08:33:10
Job time : 163 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 08:27:23 ; Search time 171 Seconds
(without alignments)
1314.636 Million cell updates/sec

Title: US-10-734-510-7

Perfect score: 2325

Sequence: 1 MVSSAFAPSLLSLSSAL.....TYARENGQGFACGFPVSE 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2325	100.0	439	2 Q96VH9	Q96vh9 peniophora
2	1204	51.8	442	2 Q96VK9	Q96vk9 cf. ceripor
3	1202	51.7	442	2 Q96VK8	Q96vk8 cf. ceripor
4	1160	49.9	443	2 Q96VF5	Q96vf5 trameses pu
5	1153	49.6	453	2 Q96VT0	Q96vt0 agroclybe pe
6	823	35.4	487	1 PHVA_THIHE	O00107 thielavia h
7	776.5	33.4	467	2 Q9HEQ0	Q9heq0 aspergillus
8	773.5	33.3	596	2 Q7S9V5	Q7s9v5 neurospora
9	769	33.1	466	2 O00096	O00096 talaromyces
10	767.5	33.0	467	2 O93838	O93838 aspergillus
11	765.5	32.9	448	2 Q8J255	Q8j255 aspergillus
12	765.5	32.9	466	2 Q9C1T1	Q9c1t1 aspergillus
13	760.5	32.7	448	2 Q6GHA8	Q6gha8 aspergillus
14	760.5	32.7	448	2 Q6J336	Q6j336 aspergillus
15	759.5	32.7	467	1 PHVA_ASPNG	P34752 aspergillus
16	758.5	32.6	467	2 Q6T9Z6	Q6t9z6 aspergillus
17	754.5	32.5	467	1 PHVA_ASPAW	P34753 aspergillus
18	749.5	32.2	467	2 Q6RS19	Q6rs19 aspergillus
19	747.5	32.2	467	2 Q9U0Z7	Q9u0z7 aspergillus
20	744	32.0	466	2 O00100	O00100 aspergillus
21	742	31.9	465	1 PHVA_ASPFU	O00092 aspergillus
22	740	31.8	442	2 Q8WZJ5	Q8wzj5 aspergillus
23	738.5	31.8	463	1 PHVB_EMENI	O00093 emericaella
24	724.5	31.2	466	1 PHVA_ASPTE	O00085 aspergillus
25	696.5	30.0	461	2 Q6YNE9	Q6yne9 penicillium
26	464	20.0	610	2 Q7SEH2	Q7seh2 neurospora
27	443.5	19.1	584	1 P6CCS5	O6ccs5 yarrowia li
28	412	17.7	463	1 PPA2_SCHPO	O01682 schizosacch
29	397	17.1	482	2 Q8X1W7	Q8x1w7 monascus an
30	390.5	16.8	463	2 Q6O172	Q6o172 schizosacch
31	390	16.8	453	1 PPA1_SCHPO	P08091 schizosacch

32	388.5	16.7	464	2 Q6BUR8	Q6bur8 debaryomyce
33	385	16.6	468	1 PPA1_PICPA	P52291 pichia past
34	356	15.3	442	2 O74677	O74677 pichia angu
35	352	15.1	479	1 PHVB_ASPNG	P34754 aspergillus
36	348	15.0	479	1 PHVB_ASPAW	P34755 aspergillus
37	345.5	14.9	467	1 PPA5_YEAST	P06635 saccharomyc
38	342	14.7	461	2 Q6BM79	Q6bm79 debaryomyce
39	335.5	14.4	463	2 Q6BM75	Q6bm75 debaryomyce
40	335.5	14.4	467	1 PPA3_YEAST	P24031 saccharomyc
41	331.5	14.3	468	1 PPA2_YEAST	P52290 saccharomyc
42	315.5	13.6	467	1 PPA8_YEAST	P35842 saccharomyc
43	312.5	13.4	467	1 PPA6_YEAST	P38693 saccharomyc
44	301.5	13.0	469	2 Q6CVI2	Q6cvi2 kluyveromyc
45	298	12.8	484	2 Q6CLW3	Q6clw3 kluyveromyc

ALIGNMENTS

RESULT 1

Q96VH9	PRELIMINARY;	PRT;	439 AA.
AC Q96VH9;			
DT 01-DEC-2001 (Tremblrel. 19, Created)			
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE Phytase precursor (EC 3.1.3.26).			
GN Name=phyA;			
OS Peniophora lycii.			
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OC Aphyllophorales; Lachnocladiaceae; Peniophora.			
OX NCBI_TaxID=154539;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21455028; PubMed=11571175;			
RX DOI=10.1128/AEM.67.10.4701-4707.2001;			
RA Lassen S.F., Breinholt J., Ostergaard P.R., Bruggner R., Bischoff A.,			
Wys M., Fuglsang C.C.;			
RT "Expression, gene cloning and characterization of five novel phytases			
RT from four basidiomycete fungi: Peniophora lycii, Agroclybe pediades, a			
RT Ceriporia sp. and Trameses pubescens.";			
RL Appl. Environ. Microbiol. 67:4701-4707(2001).			
DR EMBL; AJ310696; CAC48195.1; -.			
DR HSSP; P34752; LIHP.			
DR GO; GO:0008707; F:4-phytase activity; IEA.			
DR GO; GO:0003993; F:acid phosphatase activity; IEA.			
DR GO; GO:0016787; F:hydrolase activity; IEA.			
DR InterPro; IPR000560; Hisac.phsphtase.			
DR Pfam; PF00328; Acid_phosphat_A.1.			
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.			
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.			
FT SIGNAL	1	29	Potential.
FT CHAIN	30	439	Phytase.
SQ SEQUENCE	439 AA;	47563 MW;	F686FA9DD3839DDA CRC64;

Query Match 100.0%; Score 2325; DB 2; Length 439;

Best Local Similarity 100.0%; Pred. No. 7.3e-181;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVSSAFAPSLLSLSSALSTQSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGC	60
Db	1	MVSSAFAPSLLSLSSALSTQSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGC	60
QY	61	TYTVQNLQRHGARPSTGARSQAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF	120
Db	61	TYTVQNLQRHGARPSTGARSQAAVAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF	120
QY	121	GANQSHQGTQDMYTRYSTLFEQGDVPFVRAAGDQQRVVDSTTNWTAGFGDASGETVLTQ	180
Db	121	GANQSHQGTQDMYTRYSTLFEQGDVPFVRAAGDQQRVVDSTTNWTAGFGDASGETVLTQ	180
QY	181	VVLQEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM	240

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Db 181 VVLQEGNCTLCNNMCPNEVDGDETTWLGVFAPNITARLNAAPSANLSDSALTMDM 240
QY 241 CPFDTLSSGNASPFCDLFTAEAEVSYEYDLDKYYGTGPGNALGPVQGVYVNEILL 300
Db 241 CPFDTLSSGNASPFCDLFTAEAEVSYEYDLDKYYGTGPGNALGPVQGVYVNEILL 300
QY 301 TGOAVRDETQTNRTLSDSPATPPLNRTFYADFSDHNTMVPIFAALGLFNATLDPK 360
Db 301 TGOAVRDETQTNRTLSDSPATPPLNRTFYADFSDHNTMVPIFAALGLFNATLDPK 360
QY 361 NRLWVDSKLVPSFGHMTVEKLACSGKEAVRLVNDVAVQPLEFCGGVDGVCESAF 420
Db 361 NRLWVDSKLVPSFGHMTVEKLACSGKEAVRLVNDVAVQPLEFCGGVDGVCESAF 420
QY 421 YARENGQGDFAKCGFVPS 439
Db 421 YARENGQGDFAKCGFVPS 439

RESULT 2
Q96VK9
ID Q96VK9 PRELIMINARY; PRT; 442 AA.
AC Q96VK9;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Phytase precursor (EC 3.1.3.26).
GN Name=phyA1;
OS cf. Ceriporia sp. CBS 100231.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Ceriporia.
OX NCBI_TaxID=154783;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21455028; PubMed=11571175;
RX DOI=10.1128/AEM.67.10.4701-4707.2001;
RA Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA Wyss M., Fuglsang C.C.;
RT "Expression, gene cloning and characterization of five novel phytases
RT from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a
RT Ceriporia sp., and Trametes pubescens."
RL Appl. Environ. Microbiol. 67:4701-4707(2001).
DR EMBL; AJ310699; CAC48164.1; --
DR HSSP; P34752; 1IHP.
DR GO; GO:0008707; F:4-phytase activity; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 442 Phytase.
FT SEQUENCE 442 AA; 47915 MW; 0464C1C691D86702 CRC64;

Query Match 51.8%; Score 1204; DB 2; Length 442;
Best Local Similarity 55.3%; Pred. No. 1.6e-89;
Matches 242; Conservative 51; Mismatches 139; Indels 6; Gaps 5;

QY 1 MVSSAFAPGILLSLMSLSTQFSVAAQLPIPAQNTSNWGPDPFPPVPEYAAPPEGC 60
Db 1 MLFGFVALACLLSLSEVLATSPKN-TATFPPIPESEQRNWSFYSPFYFLAYKAPPGAC 59

QY 61 TVTVQNLIQRHGARMPTSGARQVAQVAKIOWARFPTDPKYEFLNDFVYKFGVADLLPF 120
Db 61 TVTVQNLIQRHGARMPTSGARQVAQVAKIOWARFPTDPKYEFLNDFVYKFGVADLLPF 120
QY 121 GANQSHQTGDMTRYSTLFEFGDVPFVRAAGDQVRVSDSTNWTAGFGDASGETVLP 180
Db 121 GANQSHQTGDMTRYSTLFEFGDVPFVRAAGDQVRVSDSTNWTAGFGDASGETVLP 180
QY 120 GAAQSPDAGQAEAFARYSKLVSKNLPFFIRSDGSDRVVDATNWTAGFASASNTVQPK 179
Db 120 GAAQSPDAGQAEAFARYSKLVSKNLPFFIRSDGSDRVVDATNWTAGFASASNTVQPK 179

QY 181 VVLQEGNCTLCNNMCPNEVDGDETTWLGVFAPNITARLNAAPSANLSDSALTMDM 239
Db 181 VVLQEGNCTLCNNMCPNEVDGDETTWLGVFAPNITARLNAAPSANLSDSALTMDM 239
QY 180 LILPQTGNTLEDNMCPAGDSDDPQVNAWLAVAFPSITARLNAAPSVNLTUTDAFNLS 239
Db 180 LILPQTGNTLEDNMCPAGDSDDPQVNAWLAVAFPSITARLNAAPSVNLTUTDAFNLS 239
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QY 240 MCPFDTLSSGNASPFCDLFTA--EYVSYEYDLDKYYGTGPGNALGPVQGVYVNEILL 297
Db 240 LCAFLTYSKEKKSDFCTLTFEGIPGSGFAFAYGGLDKFYGTGYGQELGPVQGVYVNELI 299

QY 298 ARLTGOAVRDETQTNRTLSDSPATPPLNRTFYADFSDHNTMVPIFAALGLFNATA-LDPL 356
Db 298 ARLTGOAVRDETQTNRTLSDSPATPPLNRTFYADFSDHNTMVPIFAALGLFNATA-LDPL 356
QY 300 ARLTNSAVRDNTQTNRTLSDSPATPPLNRTFYADFSDHNTMVPIFAALGLFNATA-LDPL 359
Db 300 ARLTNSAVRDNTQTNRTLSDSPATPPLNRTFYADFSDHNTMVPIFAALGLFNATA-LDPL 359

QY 357 KPDENRLMWDSKLVPSFGHMTVEKLACSGKEAVRLVNDVAVQPLEFCGG-VDGVCESAF 415
Db 357 KPDENRLMWDSKLVPSFGHMTVEKLACSGKEAVRLVNDVAVQPLEFCGG-VDGVCESAF 415
QY 360 VENPRTWRTSSLVPSFGHMTVEKLACSGKEAVRLVNDVAVQPLEFCGGDRNGLCTLAKF 419
Db 360 VENPRTWRTSSLVPSFGHMTVEKLACSGKEAVRLVNDVAVQPLEFCGGDRNGLCTLAKF 419

QY 416 VESQTYARENGQGDFAK 433
Db 416 VESQTYARENGQGDFAK 433
QY 420 VESQTFARSDDGADFEK 437
Db 420 VESQTFARSDDGADFEK 437

RESULT 3
Q96VK8
ID Q96VK8 PRELIMINARY; PRT; 442 AA.
AC Q96VK8;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Phytase precursor (EC 3.1.3.26).
GN Name=phyA2;
OS cf. Ceriporia sp. CBS 100231.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Ceriporia.
OX NCBI_TaxID=154783;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21455028; PubMed=11571175;
RX DOI=10.1128/AEM.67.10.4701-4707.2001;
RA Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA Wyss M., Fuglsang C.C.;
RT "Expression, gene cloning and characterization of five novel phytases
RT from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a
RT Ceriporia sp., and Trametes pubescens."
RL Appl. Environ. Microbiol. 67:4701-4707(2001).
DR EMBL; AJ310699; CAC48164.1; --
DR HSSP; P34752; 1IHP.
DR GO; GO:0008707; F:4-phytase activity; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 442 Phytase.
FT SEQUENCE 442 AA; 47552 MW; 483FAB442DB001EC CRC64;

Query Match 51.7%; Score 1202; DB 2; Length 442;
Best Local Similarity 52.6%; Pred. No. 2.4e-89;
Matches 230; Conservative 61; Mismatches 128; Indels 18; Gaps 5;

QY 2 VSSAFAPGILLSLMSLSTQFSVAAQLPIPAQNTSNWGPDPFPPVPEYAAPPEGCT 61
Db 2 VSSAFAPGILLSLMSLSTQFSVAAQLPIPAQNTSNWGPDPFPPVPEYAAPPEGCT 61
QY 14 LSEVFAASVPRN-----IAPKFSIPSEQRNWSFYSPFYFLAYKAPPGAC 60
Db 14 LSEVFAASVPRN-----IAPKFSIPSEQRNWSFYSPFYFLAYKAPPGAC 60

QY 62 TVTVQNLIQRHGARMPTSGARQVAQVAKIOWARFPTDPKYEFLNDFVYKFGVADLLPF 121
Db 62 TVTVQNLIQRHGARMPTSGARQVAQVAKIOWARFPTDPKYEFLNDFVYKFGVADLLPF 121
QY 61 INQVNIQRHGARMPTSGATRIKAGLSKLSQVQNFTDPKFDIKSFYDILGTSDLVFP 120
Db 61 INQVNIQRHGARMPTSGATRIKAGLSKLSQVQNFTDPKFDIKSFYDILGTSDLVFP 120

QY 122 ANQSHQTGDMTRYSTLFEFGDVPFVRAAGDQVRVSDSTNWTAGFGDASGETVLP 181
Db 122 ANQSHQTGDMTRYSTLFEFGDVPFVRAAGDQVRVSDSTNWTAGFGDASGETVLP 181
QY 121 AAQSPDAGLEAFARYSKLVSSDNLPPFIRSDGSDRVVDATNWTAGFASASRNAIQPKLDL 180
Db 121 AAQSPDAGLEAFARYSKLVSSDNLPPFIRSDGSDRVVDATNWTAGFASASRNAIQPKLDL 180

QY 182 VVLQEGNCTLCNNMCPNEVDGDETTWLGVFAPNITARLNAAPSANLSDSALTMDM 240
Db 182 VVLQEGNCTLCNNMCPNEVDGDETTWLGVFAPNITARLNAAPSANLSDSALTMDM 240
QY 181 ILPQTGNTLEDNMCPAGDSDDPQVNAWLAVAFPSVTAQLNAAPGANLTADAFNLVSL 240
Db 181 ILPQTGNTLEDNMCPAGDSDDPQVNAWLAVAFPSVTAQLNAAPGANLTADAFNLVSL 240
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QY 241 CPEDTLLSSGNASPPCDLFTA--PEYYSVEYDYDLDKYYGTGPGNALGPVQGVYNEILA 298
Db 241 CPMTVSKSQSKDFCTLFEGIPGSFAFAAGLDKDFYGTGYQALGPVQGVYINELLA.300
QY 299 RLITGOAVRDETOQNRITLSDSPATFPLNRTFYADFSDHNTMVPFAALGLFNATA-LDPLK 357
Db 301 RLITNSAVDNTQNRITLSDSPATFPLNRTFYADFSDHNTMVPFAALGLFNATA-LDPLK 360
QY 358 PDNRLLWVDSKLVFPGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGG-VDGVCELSAFV 416
Db 361 PDNRWLTSSVVPFARMARVERLSGAGTTKRVLVQDVQVPLEFCGGQDGLCALDKFV 420
QY 417 ESQTYARENGCGDFKAC 433
Db 421 ESQYARSGAGDFEKC 437

RESULT 4
Q96VF5 PRELIMINARY; PRT; 443 AA.
ID Q96VF5 AC Q96VF5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phytase precursor (EC 3.1.3.26).
GN Name=PhyA;
OS Trametes pubescens.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=154538;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21455028; PubMed=11571175;
RX DOI=10.1128/AEM.67.10.4701-4707.2001;
RA Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA Wyss M., Fuglsang C.C.;
RT "Expression, gene cloning and characterization of five novel phytases
RT from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a
RT Ceriporia sp., and Trametes pubescens.";
RL Appl. Environ. Microbiol. 67:4701-4707(2001).
DR EMBL: AJ310700; CAC48234.1; -.
DR HSSP: P34752; 1IHP.
DR GO: GO:0008707; F:4-phytase activity; IEA.
DR GO: GO:0003993; F:acid phosphatase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR000560; HisAc phsphtse.
DR Pfam: PF00328; Acid phosphat A; 1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 443 Phytase.
SQ SEQUENCE 443 AA; 47773 MW; 13D4BEBCE0B049D1 CRC64;

Query Match 49.9%; Score 1160; DB 2; Length 443;
Best Local Similarity 52.0%; Pred. No. 6.3e-86;
Matches 230; Conservative 63; Mismatches 127; Indels 22; Gaps 7;

QY 9 SILLSLMSSIALSTQSFVAALPIPAQNTS-----NWGPYDPEFPVPAAPP 57
Db 4 SILLASL---LFVCYAVARAVRAHIPURDTSACLDVTRDVQQSWMSVSPYFPAATVAPP 60
QY 58 ECGTVTVQVNIQRHGAWRPTSGARSRQVAAVAKIQMARPTDPKYEFLNDVYKFGVADL 117
Db 61 ASCIQNVHIIQRHGAFFPTSGAKRIQTAVAKLKAASNYTDPLLAFVNTYTSLGQDSL 120
QY 118 LPFGANQSHQGTDMYTRYSTLFEFGDVPPVRAAGDQVVDSSTNTWTAGDASGETVLP 177
Db 121 VELGATQSSBAGQEAFTYSSLSVADELFPVRAAGSDRVVATANNWTAGPALASSNITP 180
QY 178 TLOVTLQEEGNCITLCNNMCNEVDGD-ESTTWLGVFAPNITARLNAAAPSNILSDSALT 236

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Db 181 VLSVITSEAGNDTLDDNMCRAAGSDSDPQVQWLAQFAPDWTARLNAGAPCANLTDTDTYN 240
QY 237 LMDMCPFDLTSSGNASPPCDLFA--TABEYVSVEYDYDLDKYYGTGPGNALGPVQGVYV 293
Db 241 LLETCPFETFAVERSERSEFCDIYEELQAEQ--AFAYNADLDKFGYGTGYQALGPVQGVYI 298
QY 294 NELLARLTGQAVRDETOQNRITLSDSPATFPLNRTFYADFSDHNTMVPFAALGLFNATA- 352
Db 299 NELLARLTGQAVRDETOQNRITLSDSPATFPLNRTFYADFSDHNTMVPFAALGLFNATA- 358
QY 353 LDPLKPDENRLWVDSKLVFPGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGG-VDGVCE 411
Db 359 LDPTTPDPARTFLVKKIVFVSARMVVERLDCCGASQSVRLVNDVAVQPLAFCGATSGVCT 418
QY 412 LSQFVSEQTYARENGCGDFKAC 433
Db 419 LDFVSEQYARNDGEGDFEKC 440

RESULT 5
Q96VT0 PRELIMINARY; PRT; 453 AA.
ID Q96VT0 AC Q96VT0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phytase precursor (EC 3.1.3.26).
GN Name=PhyA;
OS Agrocybe pediades.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Bolbitiaceae; Agrocybe.
OX NCBI_TaxID=84607;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21455028; PubMed=11571175;
RX DOI=10.1128/AEM.67.10.4701-4707.2001;
RA Lassen S.F., Breinholt J., Ostergaard P.R., Brugger R., Bischoff A.,
RA Wyss M., Fuglsang C.C.;
RT "Expression, gene cloning and characterization of five novel phytases
RT from four basidiomycete fungi: Peniophora lycii, Agrocybe pediades, a
RT Ceriporia sp., and Trametes pubescens.";
RL Appl. Environ. Microbiol. 67:4701-4707(2001).
DR EMBL: AJ310697; CAC48160.1; -.
DR HSSP: P34752; 1IHP.
DR GO: GO:0008707; F:4-phytase activity; IEA.
DR GO: GO:0003993; F:acid phosphatase activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR000560; HisAc phsphtse.
DR Pfam: PF00328; Acid phosphat A; 1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 453 Phytase.
SQ SEQUENCE 453 AA; 49931 MW; D62F1AEFA1091E5D CRC64;

Query Match 49.6%; Score 1153; DB 2; Length 453;
Best Local Similarity 51.3%; Pred. No. 2.4e-85;
Matches 232; Conservative 61; Mismatches 135; Indels 24; Gaps 7;

QY 4 SAFAPILLSLMSLLALS--TQSFVAALPIPAQNTSNWGPYDPEFPVPAAPP 61
Db 2 SULFIGCLLVLFQASAYGVQVATFV--QFFFPQIQDSWAAVTPYVQVATPPPKDCK 59
QY 62 VTQVNIQRHGAWRPTSGARSRQVAAVAKIQMARPTDPKYEFLNDVYKFGVADLPLFG 121
Db 60 ITQVNIQRHGAWRPTSGAGTRIQAQVAKLQSAKTYTDPRLDPLTNYTYTLGHDDLVPFG 119
QY 122 ANQSHQGTDMYTRYSTLFEFGDVPPVRAAGDQVVDSSTNTWTAGDASGETVLP 181
Db 120 ALQSSQAGEETFORYSFLVSKENLPFVRSSNRVDSATNTWTEGFSAAASHVLPILFV 179
QY 182 VLQEGNCITLCNNMCNEVDGD-ESTTWLGVFAPNITARLNAAAPSNILSDSALT 240

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Db 180 ILSESNDLDDAMCFNAGSSDQGTGWTSTIYGTPIANRLNQOAPGANITAAVDSNLIPL 239
Qy 241 CPEDTLSSGNASPCFCDLFTAAEEVSYEYYDLDKTYGTGFGNALGVPVQGVYNNELLARL 300
Db 240 CAFETIVKETPSPFCNLFTPEEFAQFEYFGDLKFGYGTGQPLGVPVQGVYNNELLARL 299
Qy 301 TGOAVRDETQTNRLDSDPATFPLNRTFFYADFHDNTMVPFPAALGLFN-ATALDPLKPD 359
Db 300 TEMFVRDNTQTNRLDSSPLTFPLDRSIYADLSHDNQMIAFSAMGLFNQSSPLDPSFFN 359
Qy 360 ENRLWDSKLVPSPSGHMTVEKLAC-----SG-----KEAVRLVNDVAVOPLER 402
Db 360 PKKTWTSRUTPSPARMTVERLTCQDGTGSGGSPSRMNGNVQTFVRLVNDALQPLKF 419
Qy 403 CGG-VDGVCELSAFVESQTYARENGOGDFAKC 433
Db 420 CGGMDSLCTLEAFVESQKYARENGOGDFEKC 451

RESULT 6
PHYA_THIHE
ID -PHYA_THIHE STANDARD; PRT; 487 AA.
AC Q00107;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate 3-
DE phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate
DE phosphohydrolase A).
GN Names:PHYA;
OS Thielavia heterothallica (Myceliophthora thermophila).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Chaetomiaceae; Corynascus.
ON NCBI_TaxID=78579;
RX [1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=97177792; PubMed=9025298;
RA Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L.,
RA van Loon A.P.G.M.;
RT "The phytase subfamily of histidine acid phosphatases: isolation of
RT genes for two novel phytases from the fungi Aspergillus terreus and
RT Myceliophthora thermophila.";
RT Microbiology 143:245-252(1997).
CC -!- FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate
CC from phytate.
CC -!- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = 1D-
CC myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: Shows activity with phytic acid at a pH range of
CC 3.5 to 8.5, with maximal activity between pH 5.5 and 6.0. Also
CC accept 4-nitrophenyl phosphate as substrate with a pH optima
CC shifted to more acidic pH values.
CC -!- SIMILARITY: Belongs to the histidine acid phosphatase family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U59806; AAB52508.1; -.
DR HSP; P34752; 1IHP.
DR InterPro; IPR000560; HisAc_phsphtes.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Glycoprotein; Hydrolase; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 487 3-phytase A.
FT DOMAIN 423 433 Poly-Gly.
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FT ACT_SITE 75 75 Nucleophile (By similarity).
FT ACT_SITE 369 369 Proton donor (By similarity).
FT DISULFID 26 35 By similarity.
FT DISULFID 64 421 By similarity.
FT DISULFID 208 485 By similarity.
FT DISULFID 260 289 By similarity.
FT DISULFID 456 464 By similarity.
FT CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 247 247 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 346 346 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 487 AA; 52537 MW; 97D10EDC83D051DB CRC64;

Query Match 35.4%; Score 823; DB 1; Length 487;
Best Local Similarity 43.2%; Pred. No. 2.1e-58;
Matches 192; Conservative 52; Mismatches 142; Indels 58; Gaps 13;

Qy 41 WGPYDPFF--PVEPYAAPPEGCTVTQVNLIQHGRARWPTSGARSRQVAAVAKIQMARPPT 98
Db 43 WQGYSPYFSPSELDASIPDDCEVTFAQVLSRHGARAPTLKRAASYVDLIDRIHHGAISY 102
Qy 99 DPKYELNDVVYKFGVADLLPFGANQSHQTDVMTYSTLTFEGGDVFPVRAAGDORVVD 158
Db 103 GPGYELRTYDITLGADELTRTGQQQMVNSGKFRYRYALAR-KSIPFVRTAGQDRVVH 161
Qy 159 SSTNWTAGFGDA---SGETVLPTL---QVVLQEE--GNCTLCNNMC-----PNEVDGD 203
Db 162 SAENFTQGFHSALLADRGSTVRPTLPYDMVVIPEAGANNLHNDLCTAFESGPYSTIGD 221
Qy 204 ES-TTWLGVFAPNITARLNAAPSANLSDSALTMDMCPFFTLSS-----GN 250
Db 222 DAQDTYLSSTFAGFITARVANLPGANLTADTVALMDLCPFFETVASSSSDPADAGGN 281
Qy 251 A---SPFCDLFTABEVSVSEYVYDLDKYGTGPGNALGPVQGVYNNELLARLTQAVRD 307
Db 282 GRPLSPFRLFSESEWRAIDYVLSQVKWYGYGPNPLGTTQGVGFNNELLARLAGVPVRD 341
Qy 308 ETQTNRLDSDPATFPLNRTFYADFSDNTMTVPIFAALGLFNATALDPL-----KPDSN 361
Db 342 GTSTNRLTDGDPRTFPLGRPLYADFSDNDMMVGLGALGAYD--GVPPLDKTARRDPEEL 399
Qy 362 RLWVDSKLVPSGHMTVEKLACSG-----KEAVRLVNDVAVOPLERCGGV 406
Db 400 GGYAASAWPFAARIYVEKMRCSGGGGGGGGGGRQEKDEEMVRLVNDVRLVMTLKGCGAD 459
Qy 407 D-GVCELSAFVESQTYARENGQD 429
Db 460 ERGMCTLERFIESMAFARGNGKWD 483

RESULT 7
Q9HEQ0
ID Q9HEQ0 PRELIMINARY; PRT; 467 AA.
AC Q9HEQ0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phytase.
OS Aspergillus ficuum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5058;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., An L., Wang Y., Yuan X.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AY013315; AAG40885.1; -.
DR HSP; P34752; 1IHP.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtes.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
```


SQ SEQUENCE 467 AA; 51012 MW; 3F69AD543C0B565B CRC64;

Query Match 33.4%; Score 776.5; DB 2; Length 467;
Best Local Similarity 38.4%; Pred. No. 1.2e-54;
Matches 188; Conservative 62; Mismatches 156; Indels 83; Gaps 17;

QY 2 VSSAFAPSILLSLMSSSLALSTQSFVAALQPIPA---QNTSN-----WGP 43
DB 3 VSAVLPLLYLL-----SGTISGLAVPASRNQSTCDTVDOGYQCFSTSLHWGQ 50
QY 44 YDPPFPVPEYAA-----PPEGCTVTQVNLIRHGAQWPTSGARQVAQVAKIOMARPPFT 99
DB 51 YAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKYSALIEEIQONATTFE 110
QY 100 PKYEFNLDFYKGVADLLPFGANQSHQGTDMYTRYSTLFPEGGDVPFVRAAGDQRVDS 159
DB 111 GKYPALKTNYISLGADDLTPFGQELVNSGVKPYQRYESLTR-NIVPFIIRSSGSSRVIAS 169
QY 160 STNWTAGP-----GDASGETVLPLOVLQOE-----EGNCTLCNNMCPN 198
DB 170 GNKFIQFQSTKLDKPAQPEQSS-----PKIDVIVISEASTSNNTLDPGTCTVFED---S 221
QY 199 EVDGDESTTWLGVFAPNITARLNAAAPSAANLSDSDALTLMDMCPFDTLSSGNA-----SPF 254
DB 222 ELADDEANFTATFVPSIRQLENLDLGGVSLTDEVTYLMDCSFDTISTSTVDTKLSPP 281
QY 255 CDLFTAEYVSYEYVDLDKYYGTGPNALGPVQGVYVNNELLARLTGAQVREDETQNT 314
DB 282 CDLPFTHEEYNTDYLQSLNKYYHGAGNPLGPGTQGVGYANELLARLTGSPVHDDTSSNHT 341
QY 315 LQSDPATFPLNRTFYADFSDHNTMVPFAALGLFNATALDPLKPD--ENRLWVD---SK 368
DB 342 LQSNPATFPLNLTLYADFSDHNGDGIISLFLAUGYNGT--KPLSTTAENITQDGFSSAR 399
QY 369 LVPFSGHMTVEKLACSGKE--AVRLVNDVAVQPLEFCGGVD--GVCELSAFVESQTYARE 424
DB 400 TVPFASRMVEMVQCQSEQEPVRLVLRVNDVRVPLHCG-PVDALGRCTRDSFVKGLSFAKS 458
QY 425 NCGQDFPAK 433
DB 459 G--GDWAEC 465

RESULT 8
Q7S9V5 PRELIMINARY; PRT; 596 AA.
AC Q7S9V5;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names=NCU06351.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L.C., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryzsofova S., Rasmussen C., Metzger R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;

RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -I- CAUTION: the sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000209; EAA33149.1; -.
DR HSSP; P34752; 1IHP.
DR GO; GO:0003993; F.acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsptase.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; UNKNOWN_1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 596 AA; 65281 MW; 7085B991224AE410 CRC64;

Query Match 33.3%; Score 773.5; DB 2; Length 596;
Best Local Similarity 37.6%; Pred. No. 2.9e-54;
Matches 195; Conservative 65; Mismatches 158; Indels 101; Gaps 19;

QY 10 ILLSLMSSSLALSTQSFVAQAQ-----LPIPA-----QNTSNKGPYDPEFPVE 51
DB 82 IFVKLIMFLMVLPSYLAASLRVLSNPASCDSPELGYQCNSETHTWQYSPFSPV 141
QY 52 PYAAP--PEGCTVTQVNLIRHGAQWPTSGARQVAQVAKIOMARPPFTDPKYEFNLDFV 109
DB 142 SEISPSVPEGRLTPAQVLSRHGAREPTPGKAAASAVLTIKTISATWAPDPEFIKDY 201
QY 110 YKGVADLLPFGANQSHQGTDMYTRYSTLF---EGGDVPFVRAAGDQRVDSSTNWT 165
DB 202 YVLGVDDLTAFGQEMVNSGIKFQRYASLRDYPDPSLPFTRASQSERVIASENFTT 261
QY 166 GFQDA-----SGETVLPLOVLQOE---GNCTLCNNMC---PNEVDGDES--TWL 210
DB 262 GYSALLADKNPPPSLPLPROEMVISEPTANTNMHGLCRAFEDSTTGDAAQATFIA 321
QY 211 VFAPNITARLNAAA--PSANLSDSDALTLMDMCPFDTLT-----SGNA--SPF 254
DB 322 ANFPITARLNAAQGVTLSDTLVSLMDLCPFDTVAYPPSSSLTSSPSGSKLSPF 381
QY 255 CDLFTAEYVSYEYVDLDKYYGTGPNALGPVQGVYVNNELLARLTGAQVREDETQNT 314
DB 382 CSLFTAQDFTVYDYLQSLGKFGYGGNSLAATQGVYVNNELLARLTSPVVDNTTNT 441
QY 315 LQSDPATFPL--NRTFYADFSDHNTMVPFAALGLFNA-----TALD 354
DB 442 LDGNETDTPFLSRNRTVFADFSDHNDMMGLTALTALRIFEGVDAEKMDMTTTPREYGTGD 501
QY 355 P--LKPENRL--WYDSKLVFPFSGHMTVEKLACSG-----KEAVRVLVND 395
DB 502 PANLKEREGLFKGVV---VPPAARVYFEKMICDGDGSGEMVQSEEQDKELVRLVND 557
QY 396 AVQPLEFCGGVD--GVCELSAFVESQTYARENGQDFPAK 433
DB 558 RVVKLNGCEADBLGRCKLDKFVESMEFARRG--GDWDKC 594

RESULT 9
O00096 PRELIMINARY; PRT; 466 AA.
ID O00096;
AC O00096;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Phytase (EC 3.1.1.8).
OS Talaromyces thermophilus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Talaromyces.
OX NCBI_TaxID=28565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007872; PubMed=9349716; DOI=10.1016/S0167-4781(97)00107-3;
RA Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
RA van Loon A.P.;


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Query Match      32.9%; Score 765.5; DB 2; Length 448;
Best Local Similarity 40.7%; Pred. No. 8.9e-54;
Matches 176; Conservative 55; Mismatches 148; Indels 53; Gaps 14;

QY 41 WGPYDPFFVPEYAA-----PPEGCTVTQVNLQRHGRWPTSGARSRQVAQAKIQMARP 96
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 WQYAPFFSLANKSAISPDVPAGCQVTPAQVLSRHGARYPTDSKGKYSALIEEQONAT 88
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 97 FTDPKYEFELNDFYKFGVADLLPFGANQSHQGTDMYTRYSTLFEFGDVPFVRAAGDQRV 156
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 TEEKYAFALKTYNSLGADLLTPFGQELVNSGVKEYQRYESLTR-NIVPFISSGSSRV 147
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 157 VDSSTNWTAGF-----GDASGETVLPLOVLOE-----EGNCTLCNNM 195
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 148 IASGNKFIEGPOSTKLDKPRAPQGSS-----PKIDVISEASTSNNTLDPGCTVFED- 201
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 196 CPNEVDGDESTTWLGVFAPNITARLNAAPASANLSDSDALTLMDCMCPFTLTSSGNA--- 251
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 --SELADDIEANPTATFVSIRQLENDLSGVTLTDTETVYLMDCMCSFTISTSTVDTKL 259
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 252 SPFCDLFTAEEVSVBYVDLDKYGTGPGNALGPVQGVYNNELLARLTGQAVRDETQT 311
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 260 SPFCDLFTAEEWINYDLSLNKYYGHGAGNPLGPTQGVGYANELLARLTGSPVHDDTSS 319
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 312 NETLSDRPATFPLNRTFYADFSDHNTWPIFAALGLFNATLALDPLKPD--ENRLWD--- 366
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 320 NHTLDSNPATFPLNLTLYADFSDHNGIISILFALGLYNGT--KPLSSTTAENITQDGF 377
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 367 -SKLPFSGHMTVEKLACSGKE--AVRVLVNDVAVQPLEFCGGVD--GVCLSAFVESQTY 421
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 378 SAWTVFFASRMVYEMMQCSEQEPLVRVLVNDVRVPLHGC-PVDALGRCTRDSFKVGLSF 436
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 422 ARENGQDPAK 433
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 437 ARSG--GDWAE 446
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q9C1T1 PRELIMINARY; PRT; 466 AA.
AC Q9C1T1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phytase.
GN Name=phyA;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RA Gomi K.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042805; BAB40715.1; -.
DR HSSP; P34752; 1IHP.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN 1.
SQ SEQUENCE 466 AA; 51257 MW; 8033BED57FBA2791 CRC64;

Query Match      32.9%; Score 765.5; DB 2; Length 466;
Best Local Similarity 38.1%; Pred. No. 9.4e-54;
Matches 179; Conservative 65; Mismatches 171; Indels 55; Gaps 16;

QY 9 SILLSMSSLSLSTQPSFVAQLPIPAQNTSN-----WGPYDPFFVPEY 53
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 SVLLPITFLLS-----SVTGTPTVPSRQSCNTVDEGYQCFSVSHLMQYSPYFSDVD 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 54 AA-----PPGCTVTQVNLQRHGRWPTSGARSRQVAQAKIQMARPFPTDPKYEFELNDFV 109
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RL Nat. Struct. Biol. 4:185-190(1997).
 CC -1- FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate
 CC from phytate.
 CC -1- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = 1D-
 CC myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- BIOTECHNOLOGY: Is used as a food and feed additive. It can
 CC facilitate the degradation of phytin in soybean and other seeds
 CC used as food for monogastric animals. Sold by Novo Nordisk under
 CC the name Phytase Novo.
 CC -1- SIMILARITY: Belongs to the histidine acid phosphatase family.
 CC -----
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 CC -----
 CC EMBL; Z16414; CAA78904.1; --
 CC EMBL; M94550; AAA32705.1; --
 CC PIR; JN0482; JN0482.
 CC PDB; 1IHP; X-ray; @=30-467.
 CC InterPro; IPR000560; HisAc_phsphtse.
 CC Pfam; PF00328; Acid_phosphat_A; 1.
 CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 CC 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
 KW Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 467 3-phytase A.
 FT ACT_SITE 82 82 Nucleophile (By similarity).
 FT ACT_SITE 362 362 Proton donor (By similarity).
 FT DISULFID 31 40
 FT DISULFID 71 414
 FT DISULFID 215 465
 FT DISULFID 264 282
 FT DISULFID 436 444
 FT CARBOHYD 27 27 N-linked (GLCNAC. . .).
 FT CARBOHYD 59 59 N-linked (GLCNAC. . .).
 FT CARBOHYD 105 105 N-linked (GLCNAC. . .).
 FT CARBOHYD 120 120 N-linked (GLCNAC. . .).
 FT CARBOHYD 207 207 N-linked (GLCNAC. . .).
 FT CARBOHYD 230 230 N-linked (GLCNAC. . .).
 FT CARBOHYD 339 339 N-linked (GLCNAC. . .).
 FT CARBOHYD 352 352 N-linked (GLCNAC. . .).
 FT CARBOHYD 376 376 N-linked (GLCNAC. . .).
 FT CARBOHYD 388 388 N-linked (GLCNAC. . .).
 FT STRAND 32 33
 FT TURN 34 36
 FT STRAND 37 38
 FT TURN 40 41
 FT HELIX 42 45
 FT TURN 46 47
 FT HELIX 49 51
 FT STRAND 53 53
 FT STRAND 55 55
 FT HELIX 58 60
 FT TURN 69 70
 FT STRAND 71 81
 FT STRAND 85 85
 FT HELIX 89 105
 FT STRAND 111 118
 FT STRAND 128 128
 FT HELIX 130 146
 FT TURN 147 147
 FT HELIX 148 151
 FT TURN 152 153
 FT STRAND 157 161
 FT HELIX 164 182
 FT TURN 183 183

FT TURN 185 186
 FT TURN 189 190
 FT STRAND 196 200
 FT TURN 204 205
 FT TURN 209 210
 FT HELIX 216 220
 FT HELIX 223 233
 FT TURN 234 235
 FT HELIX 236 246
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 FT TURN 270 270
 FT HELIX 280 284
 FT HELIX 287 304
 FT TURN 305 305
 FT TURN 307 308
 FT TURN 310 312
 FT HELIX 313 316
 FT HELIX 317 328
 FT TURN 329 329
 FT HELIX 340 343
 FT TURN 346 348
 FT STRAND 355 360
 FT HELIX 362 371
 FT TURN 372 377
 FT TURN 389 394
 FT HELIX 397 400
 FT STRAND 403 403
 FT TURN 404 404
 FT STRAND 406 414
 FT TURN 421 426
 FT TURN 427 428
 FT STRAND 429 430
 FT TURN 440 441
 FT STRAND 444 445
 FT HELIX 446 452
 FT HELIX 454 457
 FT TURN 458 461
 FT HELIX 462 465
 FT TURN 466 467
 SQ SEQUENCE 467 AA; 51086 MW; 88FE8F3584341D6D CRC64;
 Query Match 32.7%; Score 759.5; DB 1; Length 467;
 Best Local Similarity 38.2%; Pred. No. 2.9e-53;
 Matches 187; Conservative 58; Mismatches 161; Indels 83; Gaps 18;
 QY 2 VSSAFAPISLLSLMSLSLSTQFSFVAAQLPIPA-QNTSN-----WGP 43
 Db 3 VSAVLLPLYLL-----SGVTSGLAVPASRNQSCDVTDOGYQCFSETSHLWGQ 50
 QY 44 YDPFFPV--EPYAAP--PEGTVTVQVNLQIRGARWPTSGARSQRVAQVAKIQMARPFTD 99
 Db 51 YAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARYPTDSKGKYSALIEEQONATTFD 110
 QY 100 PKYEELNDFVYKFGVADLLPFGANQSHQGTDMYTRYSTLFGGDVYFVRAAGDQVVD 159
 Db 111 GKYAFLLKTYNSLGADDLTPFGEQELVNSGIKFYQRYESLTR-NIVFFIRSSGSSVIAS 169
 QY 160 STNWTAGF-----GDASGETVLPTLVQVLQE-----EGNCTLCNNMCPN 198
 Db 170 GKKEGFGFQSTKLKOPRAQPGQSS-----PKIDVISEASSNNNTLDPGTCVTFED---S 221
 QY 199 EVDGDESTTWLGVFAPNITARNAAAPSANLSDSALTLMDMCPFTLSSGNA-----SPF 254
 Db 222 ELADTVANFTATFVPSIRQLENDLSGVTLTDTEVYLMDCSFDTISTSTVDTKLSPF 281
 QY 255 CDLFTAEEYVSVEYYDLDKYYGTGPGNALGPVQGVYNNELLARLTGOAVRDETQNT 314
 Db 282 CDLFTHDEWINDYLSQLSKKYYGHGAGNPLGPTQGVGYANELLARLTGSPVHDDTSSNHT 341
 QY 315 LDSDPATFPPLNRTFYADFSHDNMTWPIFAALGFNATALDPLKPD--ENRLWYD----SK 368
 Db 342 LQSSPATFPPLNSTLYADFSHDNGIISILFALGLYNGT--KPLSTTTVENTITQDGFSSAW 399

Search completed: May 27, 2005, 08:30:24
Job time : 174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 08:27:27 ; Search time 40 Seconds
(without alignments)
1055.979 Million cell updates/sec

Title: US-10-734-510-7
Perfect score: 2325
Sequence: 1 MWSSAFAPSILLSLMSLAL.....TYARENGQDFAKCGFVPSE 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	759.5	32.7	467	1 JN0656	3-phytase (EC 3.1.1.1)
2	754.5	32.5	467	1 JN0889	3-phytase (EC 3.1.1.1)
3	743.5	32.0	441	1 JN0482	3-phytase (EC 3.1.1.1)
4	412	17.7	463	2 S14119	acid phosphatase (EC 3.1.3.1)
5	390.5	16.8	463	2 T39329	thiamin-repressibl
6	390	16.8	453	1 A25326	acid phosphatase (EC 3.1.3.1)
7	385	16.6	468	2 JC4285	acid phosphatase (EC 3.1.3.1)
8	351	15.1	479	1 JN0715	3-phytase (EC 3.1.1.1)
9	348	15.0	479	1 JN0890	acid phosphatase (EC 3.1.3.1)
10	345.5	14.9	467	1 PABYC	acid phosphatase (EC 3.1.3.1)
11	335.5	14.4	467	1 PABYCC	acid phosphatase (EC 3.1.3.1)
12	331.5	14.3	468	2 S52495	acid phosphatase (EC 3.1.3.1)
13	315.5	13.6	467	2 S53476	acid phosphatase (EC 3.1.3.1)
14	312.5	13.4	467	2 S48996	acid phosphatase (EC 3.1.3.1)
15	162.5	7.0	468	2 A86233	hypothetical prote
16	159	6.8	465	2 JE0369	histidine acid pho
17	107.5	4.6	3972	2 S75251	hypothetical prote
18	104	4.5	2468	2 A83412	hypothetical prote
19	103.5	4.5	1250	2 D91018	hypothetical prote
20	103.5	4.5	1250	2 F85862	hypothetical prote
21	101.5	4.4	411	2 D88504	protein B0361.7 [i
22	101.5	4.4	1250	2 G64393	yfal protein - Esc
23	101	4.3	438	2 S64682	acid phosphatase (EC 3.1.3.1)
24	100	4.3	380	2 T16983	hypothetical prote
25	99	4.3	397	2 S52783	aspartic proteinas
26	99	4.3	415	2 T40535	probable arginine-
27	96.5	4.2	3623	2 T08618	intrinsic factor-B
28	95.5	4.1	604	2 H81110	sulfite reductase
29	95.5	4.1	770	2 S60676	cellobiose oxidase

30	95.5	4.1	926	2 D86897	hypothetical prote
31	95.5	4.1	1093	2 B86748	hypothetical prote
32	95	4.1	626	2 T41060	hypothetical ser-f
33	94.5	4.1	1335	2 H75511	DNA polymerase III
34	93.5	4.0	376	2 C84769	probable fibrillin
35	93	4.0	293	2 AB3051	hypothetical prote
36	93	4.0	300	2 B98235	fhud protein (AJ00
37	93	4.0	401	2 T37132	probable hydrolase
38	93	4.0	408	2 T20893	hypothetical prote
39	93	4.0	533	2 AG2293	hypothetical prote
40	93	4.0	629	2 AE1525	probable peptidogl
41	93	4.0	1332	2 T23024	hypothetical prote
42	92.5	4.0	343	2 T09565	peroxidase (EC 1.1
43	92.5	4.0	1321	2 T51623	aldehyde oxidase (
44	92	4.0	508	2 S64958	aspartic proteinas
45	92	4.0	713	2 JE0230	NADPH-cytochrome P

ALIGNMENTS

RESULT 1

JN0656
3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger
N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
C;Species: Aspergillus niger
C;Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0656; S28456
R;van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.F.
A.M.J.J.
Gene 127, 87-94, 1993
A;Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyA)
A;Reference number: JN0656; MUID:93252284; PMID:8387447
A;Accession: JN0656
A;Molecule type: DNA
A;Residues: 1-467 <VAN>
A;Cross-references: UNIPROT:P34752; GB:Z16414; NID:G2392; PIDN:CAA78904.1; PID:G2393
A;Experimental source: strain NRRLJ135
A;Note: parts of the sequence, including the amino end of the mature protein, were confir
C;Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and ino
C;Genetics:
A;Gene: phya
A;Introns: 15/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-467/Product: 3-phytase A #status experimental <MAT>
F;27,59,105,120,207,230,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) #stat
F;81,361/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match	32.7%	Score	759.5	DB 1	Length	467			
Best Local Similarity	38.2%	Pred. No.	9.5e-54						
Matches	187	Conservative	58	Mismatches	161	Indels	83	Gaps	18
Qy	2	VSSAFAPSILLMSLSLSTQSFVAALQPIPA-QNTSN-----	-----WGP	43					
Db	3	VSAVLLPLYLL-----SGVTSGLAVFASRNQSSCDVTQDQGYCFSETSLHGG	50						
Qy	44	YDPFFPV--EPYAAP--PEGCTVTQVNLQRHGAWPTSGARSQVAAVAKIQMARPTD	99						
Db	51	YAPFFSLANESVISPVPAGRCVTFQAQLSRHGARYPTDSKGGKYSALIEIQONATTFD	110						
Qy	100	PKYEFLNDFVYKGVADLLPFGANQSHQGTDMYTRYSTLFEAGDVPFVRAAGDQRVVD	159						
Db	111	GKVAFLKTYNSLGADLLTFPGQEQLVNSGIRKPYQYESLTR-NIVPFISSSSSRVIAS	169						
Qy	160	STNWTAGF-----GDASGETVLPFTQVLQOE-----EGNCTLCNNMCPN	198						
Db	170	GKFIIEGQSTKLKQDPAQFGQSS-----PKIDVISEASSNNNTLDPGCTVPED---S	221						
Qy	199	EVDGDESTTWLGVFAFNITARLNAAAPSANLSQSDALTMDMCPDFTLSSGNA-----SPF	254						

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Db      222 ELADTVEANFTATFVPSIRQRLENDLSGVTLTDTETVYLMDCSFDTISTSTVDTKLSPP 281
QY      255 CDLFTAEVSVSEYVYDLDKYYGTGPGNALGPVQGVYVNEILLARLTGQAVRDETQTNRT 314
Db      282 CDLFTHDEWINDYLSLKKYYGHGAGNPLGPTQGVGYANELIARLTSPVHDDTSSNHT 341
QY      315 LQSDPATFPLNRTFYADFSDHNTMVPFPAALGLFNATALDPLKPD--ENRLWVD-----SK 368
Db      342 LQSSPATFPLNSTLYADFSDHNGIISILFALGLYNGT--KPLSTTTVTENITQDGFSSAW 399
QY      369 LVPFSGHMTVEKLACSGKE--AVRVLVNDVAVPLEFCGGVD--GVCELSAFVESQTYARE 424
Db      400 TVPFASRLYVEMMQCAEQEPLRVLRVNDRVVPLHGC-FVDALGRCTRDSFVRGLSFARS 458
QY      425 NGQGDFPAK 433
Db      459 G--GDWAEC 465

RESULT 2
JN0889
3-Phytase (EC 3.1.3.8) A precursor - Aspergillus awamori
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C:Species: Aspergillus awamori
C>Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: JN0889
R:Pidgington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
Gene 133, 55-62, 1993
A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optimi
A:Reference number: JN0889; MUID:94040796; PMID:8224894
A:Accession: JN0889
A:Molecule type: DNA
A:Residues: 1-467 <PID>
A:Cross-references: UNIPROT:P34753; GB:L02421; NID:gl66518; PIDN:AAA16898.1; PID:gl66519
A:Experimental source: strain ALK0243
A:Note: part of the sequence, including the amino end of the mature protein, was confir
C:Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic pho
C:Genetics:
A:Gene: phyA
A:Introns: 15/2
A:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-467/Product: 3-phytase A #status experimental <MAT>
F:27-59,105,120,207,230,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) #sta
F:81,361/Active site: Arg. His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match      32.5%; Score 754.5; DB 1; Length 467;
Best Local Similarity 37.8%; Pred. No. 2.4e-53;
Matches 185; Conservative 61; Mismatches 160; Indels 83; Gaps 18;

QY      2 VSSAFAPSTLLSMLSLSTQSFVAAQLPIPA---QNTSN-----WGP 43
Db      3 VSAVILLPLYL-----AGVTSGLAVPAGRNQSTCTVDQGYOCFSETSHLMGQ 50
QY      44 YDPFFPV--EPYAAP--PEGCTVTQNLIRQHGAWPTSGARSQVAAVAKIQMARPFDT 99
Db      51 YAPFFSLANESALSPDPVAGCRVTPAQLVSRHGARYPTESKGGKYSALIEEQVNTTFD 110
QY      100 PKYEFNLDPVYKFGVADLLPFGANSHQGTDMYTRYSTLTFEGGDVFPVRAAGDQRVDS 159
Db      111 GKYAFLLKTYNSLIGADLLTPFGEQELVNSGIKFQRYESLTR-NIIPFIRSSGSRVIAS 169
QY      160 STNWTAGF-----GDASGETVLPLOVLOE-----EGNCTLCNNMCPN 198
Db      170 GKFTIEGFQSTKLKDPRAQPGQSS-----PKIDVWVISEASSNNNTLDPGCTCTVFED---S 221
QY      199 EYVDGESTTWLGVFAPNITARLNAAAAPSANLSDSALTLMDMCPDPTLSSGNA-----SPF 254
Db      222 ELADTVEANFTATFAPSIRQRLENDLSGVTLTDTETVYLMDCSFDTISTSTVDTKLSPP 281
QY      255 CDLFTAEVSVSEYVYDLDKYYGTGPGNALGPVQGVYVNEILLARLTGQAVRDETQTNRT 314

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Db      282 CDLFTHDEWIHYDLSLKKYYGHGAGNPLGPTQGVGYANELIARLTSPVHDDTSSNHT 341
QY      315 LQSDPATFPLNRTFYADFSDHNTMVPFPAALGLFNATALDPLKPD--ENRLWVD-----SK 368
Db      342 LQSSPATFPLNSTLYADFSDHNGIISILFALGLYNGT--KPLSTTTVTENITQDGFSSAW 399
QY      369 LVPFSGHMTVEKLACSGKE--AVRVLVNDVAVPLEFCGGVD--GVCELSAFVESQTYARE 424
Db      400 TVPFASRLYVEMMQCAEQEPLRVLRVNDRVVPLHGC-PIDALGRCTRDSFVRGLSFARS 458
QY      425 NGQGDFPAK 433
Db      459 G--GDWAEC 465

RESULT 3
JN0482
3-Phytase (EC 3.1.3.8) A - Aspergillus ficum
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C:Species: Aspergillus ficum
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: JN0482; PN0023
R:Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 747-753, 1993
A:Title: Aspergillus ficum phytase: Complete primary structure elucidation by chemical s
A:Reference number: JN0482; MUID:93249451; PMID:8387289
A:Accession: JN0482
A:Molecule type: protein
A:Residues: 1-441 <ULL>
A:Cross-references: UNIPROT:P34752
A:Note: authors state that the 9 Asn followed by Thr or Ser after an intervening residue
R:Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 178, 45-53, 1991
A:Title: Cyclonexanediene modification of arginine at the active site of Aspergillus ficu
A:Reference number: PN0023; MUID:91298982; PMID:1648914
A:Accession: PN0023
A:Molecule type: protein
A:Residues: 48-70 <UL2>
C:Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phytate.
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F:4,36,82,97,184,207,316,329,353,365/Binding site: carbohydrate (Asn) (covalent) #status
F:58,338/Active site: Arg. His #status predicted
F:59/Active site: His (phosphohistidine intermediate) #status predicted

Query Match      32.0%; Score 743.5; DB 1; Length 441;
Best Local Similarity 40.4%; Pred. No. 1.8e-52;
Matches 174; Conservative 53; Mismatches 151; Indels 53; Gaps 15;

QY      41 WGPYDPFFPV--EPYAAP--PEGCTVTQNLIRQHGAWPTSGARSQVAAVAKIQMARP 96
Db      25 WGOYAPFFSLANESVISPEVAGCRVTPAQLVSRHGARYPTDSKGGKYSALIEEQVAT 84
QY      97 FTDPKYEFNLDPVYKFGVADLLPFGANSHQGTDMYTRYSTLTFEGGDVFPVRAAGDQRV 156
Db      85 TFDGKYAFLLKTYNSLIGADLLTPFGEQELVNSGIKFQRYESLTR-NIVPFISSGSRV 143
QY      157 VDSSTNWTAGF-----GDASGETVLPLOVLOE-----EGNCTLCNNM 195
Db      144 TASGKKFTIEGFQSTKLKDPRAQPGQSS-----PKIDVWVISEASSNNNTLDPGCTCTVFED- 197
QY      196 CPNEVDGESTTWLGVFAPNITARLNAAAAPSANLSDSALTLMDMCPDPTLSSGNA---- 251
Db      198 --SELADTVEANFTATFAPSIRQRLENDLSGVTLTDTETVYLMDCSFDTISTSTVDTKL 255
QY      252 SPFCDLFTAEBYVSEYVYDLDKYYGTGPGNALGPVQGVYVNEILLARLTGQAVRDETQT 311
Db      256 SPFCDLFTHDEWINDYLSLKKYYGHGAGNPLGPTQGVGYANELIARLTSPVHDDTSS 315
QY      312 NRTLSDPATFPLNRTFYADFSDHNTMVPFPAALGLFNATALDPLKPD--ENRLWVD--- 366
Db      316 NHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGT--KPLSTTTVTENITQDGF 373

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Qy	367	-SKLVPSGHMTVEKLAACSGKE--AVRVLVNDVAOPLEFCGGVD--GVCBELSAFVESQTY	421
Ds	374	SAWTVVPASLYVEMMOCAEQEPLVRVLVNDVRVPLHGC-PVDALGRCTRDSFVRGLSF	432
Qy	422	ARENGOQDEAK	432
Ds	433	ARSG--GDWAE	441
RESULT 4			
S14119			
acid phosphatase (EC 3.1.3.2) - fission yeast (<i>Schizosaccharomyces pombe</i>)			
C;Species: Schizosaccharomyces pombe			
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004			
C;Accession: S14119; T40455			
R;Yang, J.; Schweingruber, M.E.			
Curr. Genet. 18, 269-272, 1990			
A;Title: The structural gene coding for thiamin-repressible acid phosphatase in <i>Schizosaccharomyces pombe</i>			
A;Reference number: S14119; MUID:91064763; PMID:2249257			
A;Accession: S14119			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-463 <YAN>			
A;Cross-references: UNIPROT-Q01682; GB:X56939; NID:g5006; PIDN:CAA04258.1; PID:g5007			
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.			
submitted to the EMBL Data Library, November 1998			
A;Reference number: Z21931			
A;Accession: T40455			
A;Status: preliminary; translated from GB/EMBL/DDBBJ			
A;Molecule type: DNA			
A;Residues: 1-463 <LYN>			
A;Cross-references: EMBL:AL034382; PIDN:CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03c			
A;Experimental source: strain 972h-; cosmid c428			
C;Genetics:			
A;Gene: SPBC428.03c			
A;Map position: 2			
C;Superfamily: yeast acid phosphatase			
C;Keywords: phosphoric monoester hydrolase			
Query Match 17.7%; Score 412; DB 2; Length 463;			
Best Local Similarity 32.6%; Pred. No. 1.5e-25;			
Matches 141; Conservative 58; Mismatches 168; Indels 66; Gaps 22;			
Qy	44	YDPFFPYEYAAPGECTVTQVNLIQRHGAWPTSGARSQVAAVAQIOMAR-----95	
Ds	43	HEPVFN-GPITSPESCAIKQVHLQLRHGSRNPTGDDTATDVSSAQYIDIFQNKLINGSI	101
Qy	96	PFT-----DKPIELNDF--VYKGVAD-LLPFGANOSHOTGDTMYRTSTLPEGGDVPF	147
Ds	102	VNVFSYPENPLY-FVKHWTPVIKAENADQLSSGRIELFDLGRQVFERYELEFD-TDVID	159
Qy	148	VRAAGDRVVDSNTWTAG-FGDASGETVLTLOVLQE-----GNCTLCNNCPNEVDG	202
Ds	160	INTAAQERVVDSAEEFSGMPGD---DMQNKTNFVLVPEDDSDAGANSIAMYSFCVYEYN	216
Qy	203	--DESTT-----WLGVFAFNITARLNAAAPS-A-NLSDSDALTLMDCPFDTLLSSGNASP	253
Ds	217	NIDENTTEAAHTSRWNFLKPIARNLNKYPDPSGYNLTVSDVRSYYICVVEIALRDN-SD	275
Qy	254	FCDLFTAEEYVSYYYDLKDYGTGTFGNALGPVGQVGYVVELLARLTGOAVRDETQNR	313
Ds	276	FCSLFTPSEFLNPYDSLDYAYWGGPASEWASTLGGAIVNNLANL-----RKGVNN	328
Qy	314	TLSDPATFPPLNRFYADFSDHNTWVIPFAALGF-NATALDPLKPENRLWD----SKL	369
Ds	329	ASD-----RKVFLAFTHDSQIIIVEAALGFPPDITPEHPFLTDKNIFTYSLKTSSF	379
Qy	370	VPSGHMTVEKLACS-GKEA VRVLVNDVAOPLEFC-----GGVDGVCELSAFVES--QTY	421
Ds	380	VPFAGNLITELFLCSDNKYVYRHLVNOQVPLTDTCGPGSGASDCLCELSAYLNSSVRVN	439
Qy	422	ARENGQDGF-AKC	433

A;Residues: 1-453 <ELL>
A;Cross-references: UNIPROT:P08091; GB:M11857; NID:G173422; PIDN:AAA35321.1; PID:G173423
R;Kieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25068
A;Accession: T50405
A;Molecule type: DNA
A;Residues: 1-453 <RIE>
A;Cross-references: EMBL:AL137099; PIDN:CA868657.1; GSPDB:GN00067; SPDB:SPBP4G3.02
A;Experimental source: strain 972h(-); clone pl p4G3
C;Genetics:
A;Gene: phol; SPDB:SPBP4G3.02
A;Map position: 2
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;68/Active site: Arg #status predicted
F;69/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 16.8%; Score 390; DB 1; Length 453;
Best Local Similarity 29.7%; Pred. No. 8.9e-24;
Matches 138; Conservative 58; Mismatches 190; Indels 78; Gaps 22;

QY 6 FAPSILLSSLSALSTQFS-FVA--AQLPIPAQNTSNMGPPDPFPVBPYAAPBPGCTV 62
DB 2 FLQNLFLGLAVVCANAQAFAETAFDCKDFKELTSPYHKPYF-YGPSIDFPPTCKI 60
QY 63 TQVNLQRHGAWPTSGARSQVAAVAKIQMAR-----PFTDPKYE 103
DB 61 KQVHTLQRHGRNPTGGNAADFAGVIANFQORLLNGSVPIDYSGNPLSFPTWTPVIE 120
QY 104 FLNDFYKFGVADLL-PFGANQSHQGTDMYTRYSTLFGGDPVFPVRAAGDQVVDSSNN 162
DB 121 AAN-----ADALSSGRVELFDMGQFYRYHELFASTNYITAA-QQRVVDNAL- 170
QY 163 WTAFGDSAGSETVLPQLVQLQEE-----GNCTLCNNMCPNEVDGDESTT-----WLGVF 212
DB 171 W-YGYG-MGEDVHNTNYILVSENATAGSNLSNACPAS-DADFTTPALEARNVY 227
QY 213 APNITARLNAAPSANLSDSALTMDMCPDFTLSSGNASPCDLPFAEYVSYEYDYL 272
DB 228 MPPIRQLNPFYSNYNLTDNDILNLYGICSYE-IALQDYSECKLFNSVDLFNFEYEGDL 286
QY 273 DKYQGTGNALPGVGVYVNEALLARLTGOAVRDETQTNRLDSDPATFPLNRTFYADF 332
DB 287 SFSYGMGNSVKWGSIFGGAYANSLNLSL--RSVENNTQ-----QVFFA-F 328
QY 333 SHDNTWPIFAALGLF-NATALDPLKPD---ENRLWVDSKLVPSGHMTVEKLAC-SGKE 387
DB 329 TIDANIIPVETALGFDTNPENPLPTSYQVHSHMKASEFVFFAGNLITELFQCEDSKY 388
QY 388 AVRVLVNDVAVQPLEFCG-----GVGVCELSAFVESQTYARENG 426
DB 389 YVRHLVNEEVFPLSDCGFGPSNTSDGMCELXAYLNSP--VRYNG 430

RESULT 7
JC4285
3-phytase (EC 3.1.3.2) precursor - yeast (*Pichia pastoris*)
N;Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho
C;Species: *Pichia pastoris*
C;Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4285
R;Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
Gene 163, 19-26, 1995
A;Title: An inducible acid phosphatase from the yeast *Pichia pastoris*: Characterization
A;Reference number: JC4285; MUID:96001238; PMID:7557473
A;Accession: JC4285
A;Molecule type: DNA
A;Residues: 1-468 <PAY>
A;Cross-references: UNIPROT:P52291; GB:U28658; NID:G881955; PIDN:AAA65503.1; PID:G881956
A;Experimental source: GS115
C;Genetics:
A;Gene: phol

C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-468/Product: acid phosphatase #status predicted <MAT>
F;84/Active site: His (phosphohistidine intermediate) #status predicted
F;163,196,256,321,360,453/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;345/Active site: His #status predicted

Query Match 16.6%; Score 385; DB 2; Length 468;
Best Local Similarity 29.4%; Pred. No. 2.4e-23;
Matches 143; Conservative 61; Mismatches 192; Indels 90; Gaps 23;

QY 6 FAPSILLSSLSALSTQFSFVAAQL-----PIPAQNTSNMGPPDPFPFVEPY--- 53
DB 2 FSP--ILSLEITLALATLQSFVAVELQHVGLVGNDRPYPORTDDQYNILRHGLGSPYIGY 59
QY 54 -----AAPPGCTVTVQNLQRHGAWPTSGARSQVAAVAKIQMA--RFTDPKYE 104
DB 60 NGWGIAAESEIESCTIDQAHLLMRHGERYPSTNVGKLEALYOKLLDADVEVPTGP-LSF 118
QY 105 LNDFYVKFGVADLLPF-----GANQSHQGTDMYTRYSTLTF---EGGDVPPVRAA 151
DB 119 FQD--YDFVSDAAWYEQETTKGFYSGLNTAFDFTLRERYDHLINTSEEGKLSVWAG 176
QY 152 GQORVVDSTNWTAGFGAAGETVLPQLVQLQEEG---NCTLCNNMCPN-----EVDG 202
DB 177 SQERVVDTAKYPAQCFMKSNYTDMEV--VALEEEKSQGLNSLTARISCPNYSNHYKDG 234
QY 203 DESITWLGVPAPNITA-----RLNAAAPSANLSDSALTMDMCPDFTLSSGNASPCDL 257
DB 235 D-----FPNDIAERADRLNTLSPGFNTADIPITIALYCGFELNVGRES--FCDV 284
QY 258 FTAEYVSVSEYVYDLDKYYGTGPGNALPGVGVYVNEALLARLTGOAVRDETQTNRLDS 317
DB 285 LSREALLTYALRLDGLWYVNGNPLKTYGVYAN-----ATP---QLLENTEA 332
QY 318 DPATFPLNRTFYADPSHONTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPSGHMT 377
DB 333 DPRDYPL----YFSPSHDTLQLQVFTSLGLFNVTDLPLDQIQFQTSFKSTEIVPMGARLL 388
QY 378 VEKLACS--GKEA--VRVLVNDVAVQPLEFCGCGVGV--CELSAFVESQTYARENGQDFAK 432
DB 389 TERLCTVEGEEKYVYRITLNDVAVFLSDCSSGPGFSCPLNDYVSRLEALNED--SDFAE 446
QY 433 -CGFVP 437
DB 447 NCG-VP 451

RESULT 8
JN0715
3-phytase (EC 3.1.3.8) B precursor - *Aspergillus ficum*
N;Alternate names: pH 2.5-optimum acid phosphatase
C;Species: *Aspergillus ficum*
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0715; PN0594; FN0460
R;Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
Biochem. Biophys. Res. Commun. 195, 53-57, 1993
A;Title: Identification and cloning of a second phytase gene (*phyB*) from *Aspergillus niger*
A;Reference number: JN0715; MUID:93371452; PMID:7916610
A;Accession: JN0715
A;Molecule type: DNA
A;Residues: 1-479 <EHR>
A;Cross-references: UNIPROT:P81440; GB:L20567
A;Accession: PN0594
A;Molecule type: protein
A;Residues: 20-101;133-146;376-399 <EH2>
R;Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 754-759, 1993
A;Title: Identification of active-site residues in *Aspergillus ficum* extracellular pH 2.
A;Reference number: PN0460; MUID:93249452; PMID:8484781
A;Accession: PN0460
A;Molecule type: protein

A;Residues: 65-66,68-93 <ULL>
C;Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2), has been reclassified as a phosphatase (EC 3.1.3.2), hy
C;Genetics:
A;Gene: phyB
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: Yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status experimental <MAT>
F;81.337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106.191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 15.1%; Score 351; DB 1; Length 479;
Best Local Similarity 27.9%; Pred. No. 1.4e-20;
Matches 131; Conservative 68; Mismatches 157; Indels 114; Gaps 24;
QY 11 LLSLMSSAL-STQSFVAQAQLPIPAQN-----TSNWGPYPDFPVEYAA- 55
Db 6 LUTLACALATGASAFSYGAA-IPOSTQEQFQSFQFDRDGYSLKHYGNGPYSERVSYGIA 64
QY 56 --PPEGCTTVQNLQIRHGAWPTSGARSQVAAVAKIQMARPFDTDPKYE--FLNDFVYK 111
Db 65 ROPPTGCEVDQVIMVKRHERYSPSAGKSIIEALAKVYSINT-TEYKGDLAFLNDWTY- 122
QY 112 FGVADLLP-----FGANQSHQGTMDMYTRYSTLTFEGGD-VPFVRAAGDQRV 156
Db 123 -----YVPNECYNAETTSQPYAGLLDAYNHGNDYKARYGHLWNGETVVVPPF-SSGYGRV 176
QY 157 VDSSTNWTAGDAGSETVLPVLQVVLQEGNCTLCNNMCPN-EVDGDESTTLWLVFAPN 215
Db 177 IETARKFGEGRF---FGYNYSTNAALNIISESEVMGADSLTPTCTDNDQTT-----CDN 227
QY 216 IT-----ARLNAAPSANLSDALTLMDMCPFDLTSSGNASPF---CDLFTAE 262
Db 228 LTQQLPQKFAAARLNSQNGMLTASDVYNLVWVASFEL---NARPSNWINATQDE 283
QY 263 YSYEYDYLDKYGTGPGNALGPVQGVYVNNELLARLTGQAVRDETQTNRTLDSDPATF 322
Db 284 WVSFGYVEDLNYCYCAGPGDKMAAVGAVYANASLT-LLNQGPKEA-----EAGLFPF 333
QY 323 PLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVD-----SKLVVPF 372
Db 334 NL-----AHDNTITPILAAAGV-----LIPNED-LPLDRVAFNGPYSGNIVPM 376
QY 373 SGHMTVEKLACSGKEA-----VRVLNDVAVQLEFCGGVDGV-CELSAF 415
Db 377 GGHLTIERLSQATALSDEGTYVRLVINEAVLPFNDCSTGPGYSCPLANY 426
RESULT 9
JN0890
acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0890
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
Gene 133, 55-62, 1993
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-opti
A;Reference number: JN0889; MUID:94040796; PMID:8224894
A;Accession: JN0890
A;Molecule type: DNA
A;Residues: 1-479 <PID>
A;Cross-references: UNIPROT:P34755; GB:L02420; NID:g166481; PIDN:AAA16897.1; PID:g166482
A;Experimental source: strain ALK0243
C;Comment: The highly similar enzyme from A. ficum has been shown to have 3-phytase (EC
C;Genetics:
A;Gene: aph
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status predicted <MAT>

F;81.337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106.191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 15.0%; Score 348; DB 1; Length 479;
Best Local Similarity 27.2%; Pred. No. 2.5e-20;
Matches 128; Conservative 70; Mismatches 158; Indels 114; Gaps 23;
QY 11 LLSLMSSAL-STQSFVAQAQLPIPAQN-----TSNWGPYPDFPVEYAA- 55
Db 6 LUTLACALATGASAFSYGAA-IPOSTQEQFQSFQFDRDGYSLKHYGNGPYSERVSYGIA 64
QY 56 --PPEGCTTVQNLQIRHGAWPTSGARSQVAAVAKIQMARPFDTDPKYE--FLNDFVYK 111
Db 65 ROPPTGCEVDQVIMVKRHERYSPSAGKSIIEALAKVYSINT-TEYKGDLAFLNDWTY- 122
QY 112 FGVADLLP-----FGANQSHQGTMDMYTRYSTLTFEGGD-VPFVRAAGDQRV 156
Db 123 -----YVPNECYNAETTSQPYAGLLDAYNHGNDYKARYGHLWNGETVVVPPF-SSGYGRV 176
QY 157 VDSSTNWTAGDAGSETVLPVLQVVLQEGNCTLCNNMCPN-EVDGDESTTLWLVFAPN 215
Db 177 IETARKFGEGRF---FGYNYSTNAALNIISESEVMGADSLTPTCTDNDQTT-----CDN 227
QY 216 IT-----ARLNAAPSANLSDALTLMDMCPFDLTSSGNASPF---CDLFTAE 262
Db 228 LTQQLPQKFAAARLNSQNGMLTASDVYNLVWVASFEL---NARPSNWINATQDE 283
QY 263 YSYEYDYLDKYGTGPGNALGPVQGVYVNNELLARLTGQAVRDETQTNRTLDSDPATF 322
Db 284 WVSFGYVEDLNYCYCAGPGDKMAAVGAVYANASLT-LLNQGPKEA-----SKLVVPF 372
QY 323 PLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVD-----SKLVVPF 372
Db 329 ---GSLFFFAHDNTITPILAAAGV-----LIPNED-LPLDRVAFNGPYSGNIVPM 376
QY 373 SGHMTVEKLACSGKEA-----VRVLNDVAVQLEFCGGVDGV-CELSAF 415
Db 377 GGHLTIERLSQATALSDEGTYVRLVINEAVLPFNDCSTGPGYSCPLANY 426
RESULT 10
PABYC
acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: acid phosphatase PH05; protein YBR0814; protein YBR093C
C;Species: Saccharomyces cerevisiae
C;Date: 19-Feb-1984 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S05795; A38792; S48260; S45961; A00777; A38793; S41855; B25241; A25367; A27;
R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A;Reference number: S05794; MUID:85037940; PMID:6093051
A;Accession: S05795
A;Molecule type: DNA
A;Residues: 1-467 <BAJ>
A;Cross-references: UNIPROT:P00635; EMBL:X01079; NID:g4162; PIDN:CAA25555.1; PID:g758282
A;Note: the authors translated the codon TAC for residue 272 as Thr
A;Accession: A38792
A;Molecule type: protein
A;Residues: 18-45 <BAJ>
R;Mannhaupt, G.; Stucka, R.; Ehmlé, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: S48255; MUID:95208357; PMID:7900426
A;Accession: S48260
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-467 <MAN>
A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55598.1; PID:g476051
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R;Feldmann, H.; Mannhaupt, G.; Schwarzlöse, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927

```

Qy 192 -CNWMP-----NEVDGDESTWLGVPAPNITARINAAAPSANLSDSALTMDMCPF 243
Db 211 ACNS-CPAWDYDANDDIIVNEYDTYTL-----DIAKELNKENKGLNLTSTDASTLFSWCAF 265
Qy 244 DTLSSGNASPFCDLFTAEYVSYYEYDLDKYYGTGPGNALGPVQGVGVYNELLARLTGQ 303
Db 266 EVNAKG-YSDVCDIIFTKDELVHYSYQDLHTYTHHEGPGVDIIKSVGSNLFNASVKLLKQS 324
Qy 304 AVRDETQNRTLSDSPATFPPLNRTFYADFSHDNTMVPIFAALGLFNATALDPLKPDENRL 363
Db 325 BIQDQ-----KWLSPTHDTHDIILNFLTAGIID-----DKNNL 357
Qy 364 WVDKLVPSFGH-----MTVSKLACSGKEAVRVLVNDVAVQPLFCGCGVDGV- 409
Db 358 --TAEYVFMGNTHFRSVYVPOGARVYTEKFCQSNDTYRVYVINDAVVPIETCSTGPGFS 415
Qy 410 CELSAFVESQTYARENGOG-DEAK 432
Db 416 CEINDFYD---YAEKRVAGTDFLK 436

RESULT 11
PABYCC
N/Accepted names: acid phosphatase PHO3; protein YBR0813; protein YBR092c
C/Species: Saccharomyces cerevisiae
C/Date: 30-Sep-1991 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C/Accession: S48259; S45960; S05794; A25241; S44674
R/Mannhaupt, G.; Stucka, R.; Ehnl, S.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A/Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A/Reference number: S48255; MUID:95208357; PMID:7900426
A/Accession: S48259
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-467 <MAN>
A/Cross-references: UNIPROT:P24031; EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g476050
R/Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A/Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A/Reference number: S05794; MUID:85037940; PMID:6093051
A/Accession: S05794
A/Molecule type: DNA
A/Residues: 1-218, 'MKT', 222-467 <BAJ1>
A/Cross-references: EMBL:X01080; NID:G4148; PIDN:CAA25557.1; PID:g758281
A/Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue 2
R/Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G.
Mol. Cell. Biol. 6, 1855-1865, 1986
A/Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within t
A/Reference number: A93074; MUID:87064474; PMID:3537710
A/Accession: A25241
A/Molecule type: DNA
A/Residues: 1-44 <TAI>
C/Genetics:
A/Gene: SGD:PHO3; MIPS:YBR092c
A/Cross-references: SGD:S0000296; MIPS:YBR092c
A/Map position: 2R
C/Superfamily: yeast acid phosphatase
C/Keywords: glycoprotein; phosphatidine; phosphoprotein; phosphoric monoester hydrolase
F/1-17/Domain: signal sequence #status predicted <Sig>
F/18-467/Product: acid phosphatase, constitutive #status predicted <MAT>
F/75/Active site: His (phosphatidine intermediate) #status predicted
F/97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (covalent)
F/337/Active site: His #status predicted

```

Query Match 14.4%; Score 335.5; DB 1; Length 467;
Best Local Similarity 26.3%; Pred. No. 2.5e-19;
Matches 124; Conservative 63; Mismatches 186; Indels 99; Gaps 19;

QY 21 STQSFVAALQ-----PIP---AONTNMGDPYDPFFVPEYAAP-----PEG 59
DB 4 SVVSVLAALNAGTIPIGELADVAKIGTQEDIPFPLGGAGYFSPGPGDYGISRDLP 63
QY 60 CTVTQVNLQIQRHGAWPTSGARSRQAAVAKIQMARPTDPKYEFLNDFVYKFGVA 115
DB 64 CEMKQLQMLARHGERTYPSKGTATMKTYKLSNYTRQFNGSLSLND-DYEFIRDDDD 122
QY 117 -----LLPF-GANQSHQGTDMYTRYSTLPEGGDVPFVRAAGDQVDSSTN 162
DB 123 LEMETTFANSNDVNLPTGEMDAKRAHREFLAKYKGLMENCNTNFFITNSKRIYD 179
QY 163 WTAFGDASGETVLPVLQVLOEGNCTLCNNMCP--NEVDGDE-----STWLGVPAFN 215
DB 183 FIDGLGQFNIS-LQTVSEMSAGANTLSAGNACPDWEDANDDILDKYDTTYL-----DD 237
QY 216 ISTARLNAAPSANLSDSDALTMDMCPFTLSSGNASPCDCLFTABEYYSYEEYDLDKY 275
DB 238 IAKRLKENKGLNLTSKDANTLPAWCAYE-LNARGYSVDCDIETEDLVRYSYGQDLVSP 296
QY 276 YGTGPGNALPGVGVYNELLARLTGQAVRDETQTNRLTDSDPATFPLNRTFYAFDSHD 335
DB 297 YODGPGYDMIRSVGANLFNATLKLLK-----QSETODLKV-----WLSFTHD 338
QY 336 NTWVPFAALGLFNATALDPLKDNRLWVDSKLVFPFSGH-----MTVEKLA 382
DB 339 TDLINLTAGIID-----DKNL--TABYVFMGNTFKHSYVPGARVYTEKQ 387
QY 383 CSGKEAVRLVNDVAVQLEPCGGVDGV-CELSAFVESQTYARENGQG-DPAK 432
DB 388 CSNDTVRVVINDAVVPIETCSGPGFSCIEINFDYD---YAEKRVAGTDFLK 436

RESULT 12
S52495
acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D2815
C:Species: Saccharomyces cerevisiae
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
R:Andre, B.; Visser, S.; Urrestarazu, L.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of a 42 kb segment located on the left arm of chromosome IV
A:Reference number: S52492
A:Accession: S52495
A:Molecule type: DNA
A:Residues: 1-468 <AND>
A:Cross-references: UNIPROT:P52290; EMBL:Z48432; NID:g683669; PIDN:CAA88335.1; PID:g68366
A:Experimental source: strain S288C
R:Urrestarazu, L.A.; Andre, B.; Visser, S.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67535
A:Accession: S67556
A:Molecule type: DNA
A:Residues: 1-468 <URR>
A:Cross-references: EMBL:Z74072; NID:g1430996; PIDN:CAA98583.1; PID:g1430997; MIPS:YDL02
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:DIA3
A:Cross-references: SGD:S0002182
A:Map position: 4L
C:Superfamily: yeast acid phosphatase

Query Match 14.3%; Score 331.5; DB 2; Length 468;
Best Local Similarity 27.8%; Pred. No. 5.2e-19;
Matches 128; Conservative 59; Mismatches 198; Indels 75; Gaps 23;

QY 9 SILLSSLSLSTQF-SFVAALPIPAQNT-----SNMGPDYDPFFVPEYAAP-----PEG 59

DB 8 AICLGVLKSLSIPLSRSPADIEL-IGSQKSLPFLPGGSAPYFS-PPAN-YGIFTDIEG 64
QY 60 CTVTQVNLQIQRHGAWPTSGARSRQAAVAKIQMARPTDPKYEFLNDFVYKFGVA 115
DB 65 CRLTQVMIGRHGERTYPSKGTATMKTYKLSNYTRQFNGSLSLNN-GYEFFIP 119
QY 116 D-----LLPF-GANQSHQGTDMYTRYSTLPEGGDVPFVRAAGDQVDD 158
DB 120 DESLLEMETTQNSIDVNLPTGEMDAKRAHREFLAKYKGLMENCNTNFFITNSKRIYD 179
QY 159 SSTNTWTAGFDASGETVLPVLQVLOEGNCTLCNNMCPN---EVDGDESTTWLGVPAFN 215
DB 180 TQAFPAEALGDFNIS-LQTVSEMSAGANTLSAGNACPDWEDANDDILMSVSRDYLEN 238
QY 216 ISTARLNAAPSANLSDSDALTMDMCPFTLSSGNASPCDCLFTABEYYSYEEYDLDKY 275
DB 239 ISDLNDENKGLNLTSKDAAALFSWCAPE-LNAKGYSNICDIFSAEELIHYSETDLTSF 297
QY 276 YGTGPGNALPGVGVYNELLARLTGQAVRDETQTNRLTDSDPATFPLNRTFYAFDSHD 335
DB 298 YQNGPGYKLL--IKSIG-----ANLFNATVKLIROSAH-----LDQKWLSTHD 339
QY 336 NTWVPFAALGLFN-----ATALDPLKPEDE-NRLWVDSKLVFPFSGHMTVEKLA CSKEAV 389
DB 340 TDLINLTAGIIDTTRNLTTHVFPDRHSYHRSW-----YIPQARVYTEKFOCSNDSYV 395
QY 390 RVLVNDVAVQLEPCGGVDGV-CELSAFVESQTYARENGQG 428
DB 396 RYVNDVAVVPIESSGPGFSCIEGTFYE--YAKDLRG 432

RESULT 13
S53476
acid phosphatase (EC 3.1.1.3.2) precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YAR071w
C:Species: Saccharomyces cerevisiae
C:Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kaback
submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 5'
A:Reference number: S53458
A:Accession: S53476
A:Molecule type: DNA
A:Residues: 1-467 <BUS>
R:Chen, J.Y.; Gong, Y.; AO, S.Z.
Acta Biochim. Biophys. Sin. 21, 437-444, 1989
A:Title: The primary structure of acid phosphatase gene PHO11 in S. cerevisiae and compar
A:Reference number: JCI018
A:Accession: JCI018
A:Molecule type: DNA
A:Residues: 1-16, 'L', 18-149, 'H', 151-353, 'Q', 355-422, 'G', 424-467 <CHE>
A:Note: this paper is in Chinese, with an English abstract
C:Genetics:
A:Gene: SGD:PHO11
A:Cross-references: SGD:S0000094; MIPS:YAR071w
A:Map position: 1R
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphatase #status predicted <MAT>
F;74/Active site: Arg #status predicted
F;75/Active site: His (phosphohistidine intermediate) #status predicted
F;97,162,192,250,315,356,439,445,461/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 13.6%; Score 315.5; DB 2; Length 467;
Best Local Similarity 24.1%; Pred. No. 1e-17;
Matches 115; Conservative 67; Mismatches 195; Indels 101; Gaps 17;

QY 1 MYSSAFAPISLLSLSSLSLSTQ-FSFVAALPIPAQNTSNMGPDYDPFFVPEYAAP--- 56

Db 14 LVNAGTIPLGKLSDDIKIGTQTEIFPFLGGS-----GPY-----YSPFGDY 54
QY 57 -----PEGCTVTQVNLRIQRHGAWPTSGARSRQVAAVAQIMARPTDPKYEFNLDFVY 110
Db 55 GISRDLPESCEMKQVMGHRGERTVSKAKSIMTWTYKLSNYTQFSGALSFLND-DY 113
QY 111 KFGVAD-----LLPF-GANQSHQGTGDMYTRYSTLTFEGGDVFPFVRAAGD 153
Db 114 EFFIRDTKNLEMETTLANSVNLNPTVTGEMNAKRHARDFLAQGYGVVENQTSFAVFTS 173
QY 154 ORVVDSSTNWTAGFASGETVLPLOVVLQBE---GNCTLCNNMCP---NEVDGDEST 207
Db 174 NRCHDTAQFIDGLGDKFN-----ISLOTISEAESAGANTLSAHHSCPAWDDVNDILKK 229
QY 208 WLGVFAPNITARLNAAAPSANLSDSALTMDMCPDFTLSSGNASPCFCLFTAAEEVSYE 267
Db 230 YDTKYLSGLAKLNKENKGLNLTSSDANTFFAWCAYE-INARGYSIDICNIFTKDELVRFS 288
QY 268 YYDLKYYGTGPGNALGPGVQGVYVNNELLARLTGQAVDETTQNTRLDSDPATPLNRT 327
Db 289 YGQDLETYYTGTGPGYDVRVSVGANLFNASVKLLKESEVQDQ-----K 330
QY 328 FYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWD-----SKLVPPSGHM 376
Db 331 VMLSFTHTDITLNYLTITIGIID-----DKNLTAHVPPFMENTFHRSWYVPGQARV 381
QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGV-CELSAFVESQTYARENGQG-DPAK 432
Db 382 YTEKFQCSNDTYRVYVINDVAVPIETCTGPGFSCINDFYD---YAEKRVAGTDLK 436
RESULT 14
S48996
acid phosphatase (EC 3.1.3.2) PHO12 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YHR215W
C:Species: Saccharomyces cerevisiae
C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C:Accession: S48996; S59659
R:Nacti, C.
submitted to the EMBL Data Library, February 1994
A:Description: The sequence of *S. cerevisiae* cosmid 9177.
A:Reference number: S46671
A:Accession: S48996
A:Molecule type: DNA
A:Residues: 1-467 <MAC>
A:Cross-references: UNIPROT:P38693; EMBL:U00029; NID:g551322; PIDN:AA69729.1; PID:g4589
R:Xu, L.
submitted to the EMBL Data Library, January 1995
A:Reference number: S59658
A:Accession: S59659
A:Molecule type: DNA
A:Residues: 1-16,'L',18-81,'AR',84-149,'H',151-467 <XUL>
A:Cross-references: EMBL:U19789; NID:g847754; PIDN:AAA73479.1; PID:g847755
C:Genetics:
A:Gene: SGD:PHO12
A:Cross-references: SGD:S0001258; MIPS:YHR215W
A:Map position: 8R
C:Superfamily: yeast
C:Keywords: phosphoric monoester hydrolase
Query Match 13.4%; Score 312.5; DB 2; Length 467;
Best Local Similarity 24.1%; Pred. No. 1.8e-17;
Matches 115; Conservative 66; Mismatches 196; Indels 101; Gaps 17;
QY 1 MYSSAFAPGILLSMSSLALSTQ-RSFVAAQLPIPAQNTSNWGPYDPPFPVPEYAAP--- 56
Db 14 LVNAGTIPLGKLSDDIKIGTQTEIFPFLGGS-----GPY-----YSPFGDY 54
QY 57 -----PEGCTVTQVNLRIQRHGAWPTSGARSRQVAAVAQIMARPTDPKYEFNLDFVY 110
Db 55 GISRDLPESCEMKQVMGHRGERTVSKAKSIMTWTYKLSNYTQFSGALSFLND-DY 113
QY 111 KFGVAD-----LLPF-GANQSHQGTGDMYTRYSTLTFEGGDVFPFVRAAGD 153
Db 114 EFFIRDTKNLEMETTLANSVNLNPTVTGEMNAKRHARDFLAQGYGVVENQTSFAVFTS 173
QY 154 ORVVDSSTNWTAGFASGETVLPLOVVLQBE---GNCTLCNNMCP---NEVDGDEST 207
Db 174 NRCHDTAQFIDGLGDKFN-----ISLOTISEAESAGANTLSAHHSCPAWDDVNDILKK 229
QY 208 WLGVFAPNITARLNAAAPSANLSDSALTMDMCPDFTLSSGNASPCFCLFTAAEEVSYE 267
Db 230 YDTKYLSGLAKLNKENKGLNLTSSDANTFFAWCAYE-INARGYSIDICNIFTKDELVRFS 288
QY 268 YYDLKYYGTGPGNALGPGVQGVYVNNELLARLTGQAVDETTQNTRLDSDPATPLNRT 327
Db 289 YGQDLETYYTGTGPGYDVRVSVGANLFNASVKLLKESEVQDQ-----K 330
QY 328 FYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWD-----SKLVPPSGHM 376
Db 331 VMLSFTHTDITLNYLTITIGIID-----DKNLTAHVPPFMENTFHRSWYVPGQARV 381
QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGV-CELSAFVESQTYARENGQG-DPAK 432
Db 382 YTEKFQCSNDTYRVYVINDVAVPIETCTGPGFSCINDFYD---YAEKRVAGTDLK 436

Db 114 EFFIRDTKNLEMETTLANSVNLNPTVTGEMNAKRHARDFLAQGYGVVENQTSFAVFTS 173
QY 154 ORVVDSSTNWTAGFASGETVLPLOVVLQBE---GNCTLCNNMCP---NEVDGDEST 207
Db 174 NRCHDTAQFIDGLGDKFN-----ISLOTISEAESAGANTLSAHHSCPAWDDVNDILKK 229
QY 208 WLGVFAPNITARLNAAAPSANLSDSALTMDMCPDFTLSSGNASPCFCLFTAAEEVSYE 267
Db 230 YDTKYLSGLAKLNKENKGLNLTSSDANTFFAWCAYE-INARGYSIDICNIFTKDELVRFS 288
QY 268 YYDLKYYGTGPGNALGPGVQGVYVNNELLARLTGQAVDETTQNTRLDSDPATPLNRT 327
Db 289 YGQDLETYYTGTGPGYDVRVSVGANLFNASVKLLKESEVQDQ-----K 330
QY 328 FYADFSHDNTMVPIFAALGLFNATALDPLKPDENRLWD-----SKLVPPSGHM 376
Db 331 VMLSFTHTDITLNYLTITIGIID-----DKNLTAHVPPFMENTFHRSWYVPGQARV 381
QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGV-CELSAFVESQTYARENGQG-DPAK 432
Db 382 YTEKFQCSNDTYRVYVINDVAVPIETCTGPGFSCINDFYD---YAEKRVAGTDLK 436
RESULT 15
A86233
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86233
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Mafti, R.; Marsiali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86233
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-468 <STO>
A:Cross-references: UNIPROT:O04509; GB:AE005172; NID:g2160177; PIDN:AB60740.1; GSPDB:GN
C:Genetics:
A:Map position: 1
C:Superfamily: yeast acid phosphatase
Query Match 7.0%; Score 162.5; DB 2; Length 468;
Best Local Similarity 23.2%; Pred. No. 2.7e-05;
Matches 94; Conservative 58; Mismatches 169; Indels 85; Gaps 15;
QY 57 PEGCTVTQVNLRIQRHGAWPTSGARSRQVAAVA-----KIOMARPTDPKY-----EF 104
Db 52 PSECTPIHLNLVARHGTSPK-KRLRELSLAGRKFELVRDAEARKLPDSKIPGMLGQW 110
QY 105 LNDFFVYKFGVADLLPFGANQSHQGTGDMYTRYSTLTFEGG---DVPFVRAAGDQVRVDSST 161
Db 111 KSPWEGKVGKGGELIRQGEDELQYQIRVRFPSPSFEEDYHPDVVYTIATQIPRASASAV 170
QY 162 NWTAGFGDASGETVLPLOVVLQBEQNGCTLCNNMC-PNEVDGDESTTWLGVF--APNITA 218
Db 171 AFGMG-----LFSEKGNLPGNRFAVTSNRSADTKLRFECCQNYKS 215
QY 219 RLNAAAPSANLSDSALTMDMCPDFTLSSGNASPCFCLFTAAEEVSY-----VEY 268
Db 216 YRKAKEPAVDKLEPVL-----NKITASVAKRYDLKFTKQDISSLWFLCKQVALLLEW 267
QY 269 YYDLKYYGTGPGNALGPGVQGVYVNNELLARLTGQAVDETTQNTRLDSDPATPLNRT 328
Db 268 TDDLEVFLLKGYGNSLNYKMGVPLLEDVLHSM-----EEAIKAREEKLPGSYEKAR--- 319

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 08:33:17 ; Search time 142 Seconds
(without alignments)
1066.499 Million cell updates/sec

Title: US-10-734-510-7

Perfect score: 2325

Sequence: 1 WYSSAFAPILLSLMSLAL.....TYARENGQDFAKCGFVPS 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2325	100.0	439	10	US-09-999-214-24
2	2325	100.0	439	13	US-10-083-452-7
3	2325	100.0	439	16	US-10-734-510-7
4	2325	100.0	439	17	US-10-732-923-11099
5	2254	96.9	423	15	US-10-358-960-2
6	2238	96.3	419	15	US-10-442-538-122
7	2191	94.2	409	15	US-10-442-538-145
8	2189	94.2	409	17	US-10-732-923-11118
9	1347	57.9	442	15	US-10-442-538-137
10	1204	51.8	442	10	US-09-999-214-26
11	1204	51.8	442	17	US-10-732-923-11100
12	1202	51.7	442	10	US-09-999-214-28
13	1202	51.7	442	13	US-10-083-452-4
					Sequence 24, Appli
					Sequence 7, Appli
					Sequence 11099, A
					Sequence 2, Appli
					Sequence 122, App
					Sequence 145, App
					Sequence 11118, A
					Sequence 137, App
					Sequence 26, Appl
					Sequence 11100, A
					Sequence 28, Appl

14	1202	51.7	442	16	US-10-734-510-4	Sequence 4, Appli
15	1202	51.7	442	17	US-10-732-923-11101	Sequence 11101, A
16	1201.5	51.7	422	15	US-10-442-538-119	Sequence 119, App
17	1195.5	51.4	413	15	US-10-442-538-142	Sequence 142, App
18	1191.5	51.2	422	15	US-10-442-538-118	Sequence 118, App
19	1189.5	51.2	413	15	US-10-442-538-141	Sequence 141, App
20	1160	49.9	443	10	US-09-999-214-30	Sequence 30, Appl
21	1160	49.9	443	13	US-10-083-452-5	Sequence 5, Appli
22	1160	49.9	443	16	US-10-734-510-5	Sequence 5, Appli
23	1160	49.9	443	17	US-10-732-923-11098	Sequence 11098, A
24	1155.5	49.7	420	15	US-10-442-538-120	Sequence 120, App
25	1153	49.6	453	10	US-09-999-214-22	Sequence 22, App
26	1153	49.6	453	13	US-10-083-452-6	Sequence 6, Appli
27	1153	49.6	453	16	US-10-734-510-6	Sequence 6, Appli
28	1153	49.6	453	17	US-10-732-923-11145	Sequence 11145, A
29	1150	49.5	410	15	US-10-442-538-143	Sequence 143, App
30	1148	49.4	435	15	US-10-442-538-121	Sequence 121, App
31	1144.5	49.2	425	15	US-10-442-538-144	Sequence 144, App
32	1144.5	49.2	369	15	US-10-442-538-123	Sequence 123, App
33	941.5	40.5	467	15	US-10-442-538-169	Sequence 169, App
34	831.5	35.8	467	15	US-10-442-538-139	Sequence 139, App
35	830.5	35.7	467	15	US-10-442-538-163	Sequence 163, App
36	829	35.7	457	17	US-10-492-782-42	Sequence 42, Appli
37	824.5	35.5	433	17	US-10-492-782-5	Sequence 5, Appli
38	824.5	35.5	440	17	US-10-492-782-6	Sequence 6, Appli
39	824.5	35.5	440	17	US-10-492-782-26	Sequence 26, Appli
40	824.5	35.5	440	17	US-10-492-782-27	Sequence 27, Appli
41	823	35.4	447	17	US-10-492-782-30	Sequence 30, Appli
42	823	35.4	461	17	US-10-492-782-37	Sequence 37, Appli
43	823	35.4	466	15	US-10-442-538-113	Sequence 113, App
44	823	35.4	466	15	US-10-442-538-136	Sequence 136, App
45	823	35.4	466	15	US-10-442-538-159	Sequence 159, App

ALIGNMENTS

RESULT 1
US-09-999-214-24
; Sequence 24, Application US/09999214
; Publication NO. US20030064497A1
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren P.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Giesang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/09/999,214
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/482,558
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 08/993,359
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 1481/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 0301/97
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: 0529/97
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 1388/97
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/046,082
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora lycii
; FEATURE:

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; NAME/KEY: SIGNAL
; LOCATION: (1)...(30)
US-09-999-214-24

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QY 1 MVSSAFAPSIILLMSLSTQSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGC 60
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QY 61 TTVQVNLIOHGHARWPTSGARSRQVAAVAKIQWAPFTDPKYEFLNDFYKFGVADLLPF 120
Db 61 TTVQVNLIOHGHARWPTSGARSRQVAAVAKIQWAPFTDPKYEFLNDFYKFGVADLLPF 120

QY 121 GANQSHQGTDMTRYSTLTFEGGDVPFVRAAGQQRVVDSTNTWTFAGDASGETVLTQ 180
Db 121 GANQSHQGTDMTRYSTLTFEGGDVPFVRAAGQQRVVDSTNTWTFAGDASGETVLTQ 180

QY 181 VVLOEGNCTLCNNMCPNEVDGESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM 240
Db 181 VVLOEGNCTLCNNMCPNEVDGESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM 240

QY 241 CPFDTLSSGNASPFCDLFTAEEYVSVEYYDDLDKYYGTGPGNALGPVQGVYVNEALLARL 300
Db 241 CPFDTLSSGNASPFCDLFTAEEYVSVEYYDDLDKYYGTGPGNALGPVQGVYVNEALLARL 300

QY 241 CPFDTLSSGNASPFCDLFTAEEYVSVEYYDDLDKYYGTGPGNALGPVQGVYVNEALLARL 300
Db 241 CPFDTLSSGNASPFCDLFTAEEYVSVEYYDDLDKYYGTGPGNALGPVQGVYVNEALLARL 300

QY 301 TQGAVRDEQTNRITLSDSDPATPPLNRTFYADFSHNTWMPVIFAALGLFNATALDPLKPE 360
Db 301 TQGAVRDEQTNRITLSDSDPATPPLNRTFYADFSHNTWMPVIFAALGLFNATALDPLKPE 360

QY 361 NRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDVAVQLEFCGGVDGVCESAFVESQT 420
Db 361 NRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDVAVQLEFCGGVDGVCESAFVESQT 420

QY 421 YARENGQDFAKCGFVPE 439
Db 421 YARENGQDFAKCGFVPE 439

RESULT 2
US-10-083-452-7
; Sequence 7, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora ycii
US-10-083-452-7

Query Match      100.0%; Score 2325; DB 10; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.8e-216;
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QY 61 TTVQVNLIOHGHARWPTSGARSRQVAAVAKIQWAPFTDPKYEFLNDFYKFGVADLLPF 120
Db 61 TTVQVNLIOHGHARWPTSGARSRQVAAVAKIQWAPFTDPKYEFLNDFYKFGVADLLPF 120

QY 121 GANQSHQGTDMTRYSTLTFEGGDVPFVRAAGQQRVVDSTNTWTFAGDASGETVLTQ 180
Db 121 GANQSHQGTDMTRYSTLTFEGGDVPFVRAAGQQRVVDSTNTWTFAGDASGETVLTQ 180

QY 181 VVLOEGNCTLCNNMCPNEVDGESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM 240
Db 181 VVLOEGNCTLCNNMCPNEVDGESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM 240

QY 241 CPFDTLSSGNASPFCDLFTAEEYVSVEYYDDLDKYYGTGPGNALGPVQGVYVNEALLARL 300
Db 241 CPFDTLSSGNASPFCDLFTAEEYVSVEYYDDLDKYYGTGPGNALGPVQGVYVNEALLARL 300

QY 301 TQGAVRDEQTNRITLSDSDPATPPLNRTFYADFSHNTWMPVIFAALGLFNATALDPLKPE 360
Db 301 TQGAVRDEQTNRITLSDSDPATPPLNRTFYADFSHNTWMPVIFAALGLFNATALDPLKPE 360

QY 361 NRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDVAVQLEFCGGVDGVCESAFVESQT 420
Db 361 NRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDVAVQLEFCGGVDGVCESAFVESQT 420

QY 421 YARENGQDFAKCGFVPE 439
Db 421 YARENGQDFAKCGFVPE 439

RESULT 3
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; Sequence 7, Application US/10734510
; Publication No. US20040175376A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/734,510
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US/09/273,871A
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora ycii
US-10-734-510-7

Query Match      100.0%; Score 2325; DB 16; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.8e-216;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MVSSAFAPSTLLSMLSSALSTQFSFVAAQLPIPAQNTSNMGYPDPFPVPEVYAAPPEG 60
Db 1 MVSSAFAPSTLLSMLSSALSTQFSFVAAQLPIPAQNTSNMGYPDPFPVPEVYAAPPEG 60
QY 61 TVTVQVNLIORHGAWPTSGARSRQVAQVAKIQMARPTDPKYEFLNDFVYKFGVADLLPF 120
Db 61 TVTVQVNLIORHGAWPTSGARSRQVAQVAKIQMARPTDPKYEFLNDFVYKFGVADLLPF 120
QY 121 GANQSHQGTGDMTRYSTLTFEGGDVFPVRAAGQQRVVDSTNWTAGFGDASGETVLP TLQ 180
Db 121 GANQSHQGTGDMTRYSTLTFEGGDVFPVRAAGQQRVVDSTNWTAGFGDASGETVLP TLQ 180
QY 181 VVLQEGNCTLCNNMCPNEVDGDETTWLGVPAPNITARLNAAAPSANLSDSALTLMDM 240
Db 181 VVLQEGNCTLCNNMCPNEVDGDETTWLGVPAPNITARLNAAAPSANLSDSALTLMDM 240
QY 241 CPDPTLSSGNASPFCDLFTAEEYVSVEYYDLDKYGTGPGNALGVPQGVGYVNEILLARL 300
Db 241 CPDPTLSSGNASPFCDLFTAEEYVSVEYYDLDKYGTGPGNALGVPQGVGYVNEILLARL 300
QY 301 TGOAVRDETQTRNLDSDPATPFLNRTFYADPFSHDNTMVP IFAALGLFNATLDP LKPD 360
Db 301 TGOAVRDETQTRNLDSDPATPFLNRTFYADPFSHDNTMVP IFAALGLFNATLDP LKPD 360
QY 361 NRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQT 420
Db 361 NRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQT 420
QY 421 YARENGQGDFAKCGFVPE 439
Db 421 YARENGQGDFAKCGFVPE 439

RESULT 4

US-10-732-923-11099
; Sequence 11099, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 11099
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora lycii

US-10-732-923-11099

Query Match 100.0%; Score 2325; DB 17; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.8e-216;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAFAPSTLLSMLSSALSTQFSFVAAQLPIPAQNTSNMGYPDPFPVPEVYAAPPEG 60
Db 1 MVSSAFAPSTLLSMLSSALSTQFSFVAAQLPIPAQNTSNMGYPDPFPVPEVYAAPPEG 60
QY 61 TVTVQVNLIORHGAWPTSGARSRQVAQVAKIQMARPTDPKYEFLNDFVYKFGVADLLPF 120
Db 61 TVTVQVNLIORHGAWPTSGARSRQVAQVAKIQMARPTDPKYEFLNDFVYKFGVADLLPF 120
QY 121 GANQSHQGTGDMTRYSTLTFEGGDVFPVRAAGQQRVVDSTNWTAGFGDASGETVLP TLQ 180
Db 121 GANQSHQGTGDMTRYSTLTFEGGDVFPVRAAGQQRVVDSTNWTAGFGDASGETVLP TLQ 180
QY 181 VVLQEGNCTLCNNMCPNEVDGDETTWLGVPAPNITARLNAAAPSANLSDSALTLMDM 240
Db 181 VVLQEGNCTLCNNMCPNEVDGDETTWLGVPAPNITARLNAAAPSANLSDSALTLMDM 240
QY 241 CPDPTLSSGNASPFCDLFTAEEYVSVEYYDLDKYGTGPGNALGVPQGVGYVNEILLARL 300

Db 241 CPDPTLSSGNASPFCDLFTAEEYVSVEYYDLDKYGTGPGNALGVPQGVGYVNEILLARL 300
QY 301 TGOAVRDETQTRNLDSDPATPFLNRTFYADPFSHDNTMVP IFAALGLFNATLDP LKPD 360
Db 301 TGOAVRDETQTRNLDSDPATPFLNRTFYADPFSHDNTMVP IFAALGLFNATLDP LKPD 360
QY 361 NRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQT 420
Db 361 NRLWVDSKLVPPSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQT 420
QY 421 YARENGQGDFAKCGFVPE 439
Db 421 YARENGQGDFAKCGFVPE 439

RESULT 5

US-10-358-960-2
; Sequence 2, Application US/10358960
; Publication No. US20030208788A1
; GENERAL INFORMATION:
; APPLICANT: Matsui, Tomoko
; APPLICANT: Fugisang, Claus
; APPLICANT: Svendsen, Allan
; APPLICANT: Fukuyama, Shiro
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 10261.200-US
; CURRENT APPLICATION NUMBER: US/10/358,960
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Peniophora lycii

US-10-358-960-2

Query Match 96.9%; Score 2254; DB 15; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.3e-209;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 SLALSTQFSFVAAQLPIPAQNTSNMGYPDPFPVPEVYAAPPEGCTVTQVNLIORHGAWP 76
Db 1 SLALSTQFSFVAAQLPIPAQNTSNMGYPDPFPVPEVYAAPPEGCTVTQVNLIORHGAWP 60
QY 77 TSGARSRQVAQVAKIQMARPTDPKYEFLNDFVYKFGVADLLPFPGANQSHQGTGDMTRY 136
Db 61 TSGARSRQVAQVAKIQMARPTDPKYEFLNDFVYKFGVADLLPFPGANQSHQGTGDMTRY 120
QY 137 STLFEFGGDVFPVRAAGQQRVVDSTNWTAGFGDASGETVLP TLQVVLQEGNCTLCNNMC 196
Db 121 STLFEFGGDVFPVRAAGQQRVVDSTNWTAGFGDASGETVLP TLQVVLQEGNCTLCNNMC 180
QY 197 PNEVDGDETTWLGVPAPNITARLNAAAPSANLSDSALTLMDMCPDPTLSSGNASPFCD 256
Db 181 PNEVDGDETTWLGVPAPNITARLNAAAPSANLSDSALTLMDMCPDPTLSSGNASPFCD 240
QY 257 LFTAEEYVSVEYYDLDKYGTGPGNALGVPQGVGYVNEILLARLTGOAVRDETQTRNLTD 316
Db 241 LFTAEEYVSVEYYDLDKYGTGPGNALGVPQGVGYVNEILLARLTGOAVRDETQTRNLTD 300
QY 317 SDPATPFLNRTFYADPFSHDNTMVP IFAALGLFNATLDP LKPDENLWVDSKLVPPSGHM 376
Db 301 SDPATPFLNRTFYADPFSHDNTMVP IFAALGLFNATLDP LKPDENLWVDSKLVPPSGHM 360
QY 377 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQTYARENGQGDFAKCGFV 436
Db 361 TVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQTYARENGQGDFAKCGFV 420
QY 437 PSE 439
Db 421 PSE 423

```
RESULT 6
US-10-442-538-122
; Sequence 122, Application US/10442538
; Publication No. US20030224491A1
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/10/442,538
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; TYPE: PRT
; ORGANISM: P. lycin
US-10-442-538-122

Query Match          96.3%; Score 2238; DB 15; Length 419;
Best Local Similarity 100.0%; Pred. No. 4.5e-208;
Matches 419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 STQFSVAALPIPAQNTSNMGYPDPFFVEPYAAPPEGCTTQVNLQIRHGARWPTSGA 80
DB 1 STQFSVAALPIPAQNTSNMGYPDPFFVEPYAAPPEGCTTQVNLQIRHGARWPTSGA 60

QY 81 RSRQVAANAQIOMARPFDPKYEFLNDFYKFGVADLLPFGANQSHQGTDMYTRYSTLF 140
DB 61 RSRQVAANAQIOMARPFDPKYEFLNDFYKFGVADLLPFGANQSHQGTDMYTRYSTLF 120

QY 141 EGGDVPFVRAAGQQRVDSSTNTWAGFDASGETVLPQLQVVLQEEGNCCTLCNNMCPNEV 200
DB 121 EGGDVPFVRAAGQQRVDSSTNTWAGFDASGETVLPQLQVVLQEEGNCCTLCNNMCPNEV 180

QY 201 DGEESTWLGVPAPNITARLNAAPSAANLSDSALTLMDMCPDFTLSSGNASPFCDLFTA 260
DB 181 DGEESTWLGVPAPNITARLNAAPSAANLSDSALTLMDMCPDFTLSSGNASPFCDLFTA 240

QY 261 EYVSVYDYDLDKYGTGPGNAGVQGVVNNELLARLTGQAVRDETQTNRTLSDPA 320
DB 241 EYVSVYDYDLDKYGTGPGNAGVQGVVNNELLARLTGQAVRDETQTNRTLSDPA 300

QY 321 TPPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEK 380
DB 301 TPPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEK 360

QY 381 LACSGKEARVLVNDVQPLEFCGGVGVCELSAFVESQTYARENGQGDFAKCGFVPS 439
DB 361 LACSGKEARVLVNDVQPLEFCGGVGVCELSAFVESQTYARENGQGDFAKCGFVPS 419

RESULT 7
US-10-442-538-145
; Sequence 145, Application US/10442538
; Publication No. US20030224491A1
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/10/442,538
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
```

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; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 409
; TYPE: PRT
; ORGANISM: P. lycin
US-10-442-538-145

Query Match          94.2%; Score 2191; DB 15; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.6e-203;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 LPIPAQNTSNMGYPDPFFVEPYAAPPEGCTTQVNLQIRHGARWPTSGARQVAANAK 90
DB 1 LPIPAQNTSNMGYPDPFFVEPYAAPPEGCTTQVNLQIRHGARWPTSGARQVAANAK 60

QY 91 IQMARPFDPKYEFLNDFYKFGVADLLPFGANQSHQGTDMYTRYSTLFEFGDVPFVRA 150
DB 61 IQMARPFDPKYEFLNDFYKFGVADLLPFGANQSHQGTDMYTRYSTLFEFGDVPFVRA 120

QY 151 AGDQRVVDSSTNTWAGFDASGETVLPQLQVVLQEEGNCCTLCNNMCPNEVDGESTWLG 210
DB 121 AGDQRVVDSSTNTWAGFDASGETVLPQLQVVLQEEGNCCTLCNNMCPNEVDGESTWLG 180

QY 211 VFAPNITARLNAAPSAANLSDSALTLMDMCPDFTLSSGNASPFCDLFTAEEYVSEY 270
DB 181 VFAPNITARLNAAPSAANLSDSALTLMDMCPDFTLSSGNASPFCDLFTAEEYVSEY 240

QY 271 DLDKYGTGPGNAGVQGVVNNELLARLTGQAVRDETQTNRTLSDPATPLNRTFYA 330
DB 241 DLDKYGTGPGNAGVQGVVNNELLARLTGQAVRDETQTNRTLSDPATPLNRTFYA 300

QY 331 DFDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEKLCSGKEAVR 390
DB 301 DFDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEKLCSGKEAVR 360

QY 391 VLVDVAVQPLEFCGGVGVCELSAFVESQTYARENGQGDFAKCGFVPS 439
DB 361 VLVDVAVQPLEFCGGVGVCELSAFVESQTYARENGQGDFAKCGFVPS 409

RESULT 8
US-10-732-923-11118
; Sequence 1118, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 11118
; LENGTH: 409
; TYPE: PRT
; ORGANISM: synthetic construct
US-10-732-923-11118

Query Match          94.2%; Score 2189; DB 17; Length 409;
Best Local Similarity 99.8%; Pred. No. 2.5e-203;
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 31 LPIPAQNTSNMGYPDPFFVEPYAAPPEGCTTQVNLQIRHGARWPTSGARQVAANAK 90
DB 1 MPIPAQNTSNMGYPDPFFVEPYAAPPEGCTTQVNLQIRHGARWPTSGARQVAANAK 60

QY 91 IQMARPFDPKYEFLNDFYKFGVADLLPFGANQSHQGTDMYTRYSTLFEFGDVPFVRA 150
DB 61 IQMARPFDPKYEFLNDFYKFGVADLLPFGANQSHQGTDMYTRYSTLFEFGDVPFVRA 120
```

Qy	151	AGDQVVDSSNTWTAGFDASGETVPLTQVVLQBEQNGCTLCNNMCPNEVDGDESTTWLG	210
Db	121	AGDQVVDSSNTWTAGFDASGETVPLTQVVLQBEQNGCTLCNNMCPNEVDGDESTTWLG	180
Qy	211	VFAFNIITARLNAAPASAMLSDSDALTLMDMCPFDLTSSGNASPFCDLFTAEEVVSVEYYY	270
Db	181	VFAFNIITARLNAAPASAMLSDSDALTLMDMCPFDLTSSGNASPFCDLFTAEEVVSVEYYY	240
Qy	271	DLDKYGTGPGNALGPVQGVGYVNEELLARLTGQAVRDETQTNRTLTDSDPATPLNRTFYA	330
Db	241	DLDKYGTGPGNALGPVQGVGYVNEELLARLTGQAVRDETQTNRTLTDSDPATPLNRTFYA	300
Qy	331	DFSHDNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPSFGHMTVEKLACSGKEAVR	390
Db	301	DFSHDNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPSFGHMTVEKLACSGKEAVR	360
Qy	391	VLNVDAVQPLEFCGGVDGVCBSLAFVESQTYARENGQGDFAKCGFVPSE	439
Db	361	VLNVDAVQPLEFCGGVDGVCBSLAFVESQTYARENGQGDFAKCGFVPSE	409

RESULT 9

```

US-10-442-538-137
; Sequence 137, Application US/10442538
; Publication No. US20030224491A1
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/10/442,538
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Basidio
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(442)
; OTHER INFORMATION: n is unknown
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(442)
; OTHER INFORMATION: x is unknown
US-10-442-538-137

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	Query Match	57.9%;	Score 1347;	DB 15;	Length 442;
	Best Local Similarity	61.8%;	Pred. No. 1.4e-121;		
	Matches 267;	Conservative 32;	Mismatches 111;	Indels 22;	Gaps 5;
Qy	28	AAQLPIPAQNTSNNGPDPDPFPFVPAAPBEGCTVTQVNIQIRHGAWPMSGARSRVAA	87		
Db	9	AAQLPIPXQXQXWSPSPFPVVAAXYAPGACQIXQVNIQIRHGAWPMSGATRIQAA	68		
Qy	88	VAKIQMARPTDPKYEFINDFVYKFGVADLLPFGANOSHQTGTDMYTRYSTLFFGSDVPF	147		
Db	69	VAKIQSAXXTPDKPLDFLXNXTYXGLGXDDLVPFGAXOSSQAGFAFTRYSLVSLXNDLPP	128		
Qy	148	VRAAGDORVVDSSNTWTATAGDFGASGETVLPLOVVLQEBEGNCTLCNNMCNPEVDGD--EST	206		
Db	129	VRAAGSDRVVDSSNTWTATGAFAXASXNTYXPXLXVILSEXGNDTLDDNNCPXAGSDPQXN	188		
Qy	207	TWLGVPAPNITARLNAAPASNLSDSDALTLMDMCPFDTTSSGNASPFCDLF--TAEYV	264		
Db	189	XWLAVAFAPPTARLNAAPAGANITDXDAXNLXLCPPETVSXEXKSYFCOLFEXXPPFEFX	248		

[illegible]

RESULT 10

```

US-09-999-214-26
; Sequence 26, Application US/09999214
; Publication No. US20030064497A1
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens C.
; APPLICANT: Ostersgaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/09/999,214
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/482,558
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 08/993,359
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 1481/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 0301/97
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: 0529/97
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 1388/97
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/046,082
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involutus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) .. (19)
US-09-999-214-26

```

	Query Match	51.8%	Score 1204;	DB 10;	Length 442;
	Best Local Similarity	55.3%;	Pred. NO. 1.1e-107;		
	Matches 242;	Conservative 51;	Mismatches 139;	Indels 6;	Gaps 5;
Qy	1	MVSSAAPSFTLLISMGSLLALSTQSFVAAQLPIPAQNTSNWGPVDFPFPVEPYAAPGCG	60		
Db	1	MLRFGFVALCCLLSSEVLATSVKPN-TAPTFPIPESEQRNWSVPFPFLAEYKAPAGC	59		
Qy	61	TVTVQVNLIRQHGRWPSTSGARSQVAAVAKIQMARPTDPKYEPLNDFVYKFGVADLLPF	120		
Db	60	QINQVNLIRQHGRFPPTSGATTRIKAGLTKLQGVQNTDAKFNFKSFKYDLGNSDLVPP	119		
Qy	121	GANQSHQTGDMTRYSTLTLEGGDVPPVRAAGDQORVVDSTNNWTAGFGDASGETVLTQL	180		
Db	120	GAAQSDPDAGQEAARYSKLVSKNLPPIRADGSDRVVDSATNNWTAGFSASHNTVQPKLN	179		


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RESULT 15
US-10-732-923-11101
; Sequence 11101, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 11101
; LENGTH: 442
; TYPE: PRT
; ORGANISM: cf. Ceriporia sp. CBS 100231
US-10-732-923-11101

Query Match      51.7%; Score 1202; DB 17; Length 442;
Best Local Similarity 52.6%; Pred. No. 1.7e-107;
Matches 230; Conservative 61; Mismatches 128; Indels 18; Gaps 5;

Qy      2 VSSAFAPSIILLSSLSIALSTQSFVAAQLPIPAQNTSNWGPYDPPFPVPEYAAPPEGCT 61
Db      14 LSEVFAASVPRN-----IAPKFSIPESQRNWSPYSPYFPLAEYKAPPAGCE 60

Qy      62 VTQVNLIQRHGARWPTSGARSQVAAVAKIQMARPTDPKYBFLNDFVYKFGVADLLPFG 121
Db      61 INQVNLIQRHGARFPFTSGAATRIKAGLSKLQSVQNFDPKDFIKSFYDLGTSDDLVPFG 120

Qy      122 ANQSHQTGDMYTRYSTLFEFGDVPFVRAAGQORVVDSSTNWTAGFGDASGETVLPFLQV 181
Db      121 AAQSPDAGLEVFAFYSKLVSSDNLPEIRSDGSDRVVDATNWTAGFASRNAIQPKLDL 180

Qy      182 VLQEEGNCITLCNNMCPNEVDGD--ESTTWLGVFAPNITARLNAAAAPSANLSDSALTMDM 240
Db      181 ILPQTGNDTLEONMCPAAGESDPQVDWLASAPPSVTAQINAAAAPGANLTDADFNLVSL 240

Qy      241 CPFDTLSSGNASPFCDLFTA--EEVVSVEYYDLDKYGTGPGNALGPVQGVYNELIA 298
Db      241 CPFTVTSKEQKSDFCITLFBGIPGSFEAFAYAGDLDFYGTGYGQALGPVQGVYNELIA 300

Qy      299 RLTGQAVRDETQTNRTLDSDPATFPLNRTFYADFSHDNTMTVPFI AALGLFNATA-LDPLK 357
Db      301 RLTN SAVNDNTQTNRTLDAAPDTFPLNKTMYADFSDHNLWAVFSAMGLFRQSAPLSTST 360

Qy      358 PDENRLWVDSKLVPSGHTVKEKACSGEAVRVLVNDVQPLEFCGG--VDGVCELSAEV 416
Db      361 PDNRTWLTSVVVPSFARWAVERLSCAGTKRVVLVQDQVQPLEFCGGQDGLCALDKFV 420

Qy      417 ESQTYARENGQGDFAKC 433
Db      421 ESQAYARSGAGDFEKC 437
```

Search completed: May 27, 2005, 08:46:20
Job time : 144 secs

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OM protein - protein search, using sw model

Run on: May 27, 2005, 08:27:27 ; Search time 43 Seconds
(without alignments)
762.115 Million cell updates/sec

Title: US-10-734-510-7
Perfect score: 2325
Sequence: 1 MVSSAFAPSIILLSSLSLAL.....TYARENGQGFPAKGFVPSE 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/6C COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2325	100.0	439	3	US-08-993-359-24
2	2325	100.0	439	3	US-09-221-654-2
3	2325	100.0	439	3	US-08-989-358A-2
4	2325	100.0	439	4	US-09-273-871A-7
5	2325	100.0	439	4	US-09-482-558A-24
6	2325	100.0	439	4	US-10-083-452-7
7	2238	96.3	419	4	US-09-684-855-122
8	2238	96.3	419	4	US-09-488-265B-21
9	2191	94.2	409	4	US-09-684-855-145
10	1347	57.9	442	4	US-09-684-855-137
11	1204	51.8	442	3	US-08-993-359-26
12	1204	51.8	442	4	US-09-482-558A-26
13	1202	51.7	442	3	US-08-993-359-28
14	1202	51.7	442	4	US-09-273-871A-4
15	1202	51.7	442	4	US-09-482-558A-28
16	1202	51.7	442	4	US-10-083-452-4
17	1201.5	51.7	422	4	US-09-684-855-119
18	1201.5	51.7	422	4	US-09-488-265B-18
19	1195.5	51.4	413	4	US-09-684-855-142
20	1191.5	51.2	422	4	US-09-684-855-118
21	1191.5	51.2	422	4	US-09-488-265B-17
22	1189.5	51.2	422	4	US-09-684-855-141
23	1160	49.9	443	3	US-08-993-359-30
24	1160	49.9	443	4	US-09-273-871A-5
25	1160	49.9	443	4	US-09-482-558A-30
26	1160	49.9	443	4	US-10-083-452-5
27	1155.5	49.7	420	4	US-09-684-855-120

28	1155.5	49.7	420	4	US-09-488-265B-19	Sequence 19, Appl
29	1153	49.6	453	3	US-08-993-359-22	Sequence 22, Appl
30	1153	49.6	453	4	US-09-273-871A-6	Sequence 6, Appl1
31	1153	49.6	453	4	US-09-482-558A-22	Sequence 22, Appl1
32	1153	49.6	453	4	US-10-083-452-6	Sequence 6, Appl1
33	1150	49.5	410	4	US-09-684-855-143	Sequence 143, App
34	1149	49.4	435	4	US-09-684-855-121	Sequence 121, App
35	1149	49.4	435	4	US-09-488-265B-20	Sequence 20, Appl
36	1148	49.4	425	4	US-09-684-855-144	Sequence 144, App
37	1144.5	49.2	369	4	US-09-684-855-123	Sequence 123, App
38	1144.5	49.2	369	4	US-09-488-265B-22	Sequence 22, Appl
39	941.5	40.5	467	4	US-09-684-855-169	Sequence 169, App
40	941.5	40.5	467	4	US-09-488-265B-36	Sequence 36, Appl
41	831.5	35.8	441	4	US-09-488-265B-24	Sequence 24, Appl
42	831.5	35.8	467	4	US-09-684-855-139	Sequence 139, App
43	831.5	35.8	467	4	US-09-488-265B-26	Sequence 26, Appl
44	830.5	35.7	467	4	US-09-684-855-163	Sequence 163, App
45	830.5	35.7	467	4	US-09-488-265B-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-08-993-359-24
; Sequence 24, Application US/08993359A
; Patent No. 6039942
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Ostersgaard, Claus C.
; APPLICANT: Fugisang, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/08/993,359A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 1480/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 1481/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 0301/97
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 0529/97
; EARLIER FILING DATE: 1997-05-07
; EARLIER APPLICATION NUMBER: 1388/97
; EARLIER FILING DATE: 1997-12-01
; EARLIER APPLICATION NUMBER: 60/046,082
; EARLIER FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora lycii
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(30)
US-08-993-359-24

Query Match	100.0%;	Score 2325;	DB 3;	Length 439;
Best Local Similarity	100.0%;	Pred. No. 2.7e-250;		
Matches 439;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MVSSAFAPSIILLSMSLSLALSTQSFVAAQLPTPAQNTSNWGPYDFFPVEPYAAPPEGC	60	
Db	1	MVSSAFAPSIILLSMSLSLALSTQSFVAAQLPTPAQNTSNWGPYDFFPVEPYAAPPEGC	60	
Qy	61	TVTVQVNLIRHGHWPTSGARSRQVAAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF	120	
Db	61	TVTVQVNLIRHGHWPTSGARSRQVAAKIQMARPFTDPKYEFLNDFVYKFGVADLLPF	120	

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QY 121 GANQSHQTGDMTRYSTLFEQGVDPFVRAAGDQVRVDSSTNTWTAAGDASGETVLTQ 180
Db 121 GANQSHQTGDMTRYSTLFEQGVDPFVRAAGDQVRVDSSTNTWTAAGDASGETVLTQ 180
QY 181 VVLQEGNCTLCNNMCNEVDGDESTTLGVEFAPNITARLNAAAPSANLSDSALTMDM 240
Db 181 VVLQEGNCTLCNNMCNEVDGDESTTLGVEFAPNITARLNAAAPSANLSDSALTMDM 240
QY 241 CPFDTLSSGNASPFCDLFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVGYVNEILLARL 300
Db 241 CPFDTLSSGNASPFCDLFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVGYVNEILLARL 300
QY 301 TGOAVRDETQTNRTLDSDPATFPLNRTFYADPFSHNTMVPIFAALGLFNATLDPKPD 360
Db 301 TGOAVRDETQTNRTLDSDPATFPLNRTFYADPFSHNTMVPIFAALGLFNATLDPKPD 360
QY 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVQPLEFCGGVGVCELSAFVESQT 420
Db 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVQPLEFCGGVGVCELSAFVESQT 420
QY 421 YARENGQGDFAKCGFVPSE 439
Db 421 YARENGQGDFAKCGFVPSE 439

RESULT 2
US-09-221-654-2
; Sequence 2, Application US/09221654
; Patent No. 6054306
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren
; APPLICANT: Bech, Lisbeth
; APPLICANT: Fuglsang, Claus
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Ostergaard, Peter
; TITLE OF INVENTION: Peniophora Phytase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6054306 No. 6054306disk of No. 6054306th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,654
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,358
; FILING DATE: 12-DEC-1997
; APPLICATION NUMBER: 0529/97
; FILING DATE: 07-MAY-1997
; APPLICATION NUMBER: 60/046,081
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5101.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-221-654-2

Query Match 100.0%; Score 2325; DB 3; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAFAPSIILSLSSALSTQSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGC 60
Db 1 MVSSAFAPSIILSLSSALSTQSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEGC 60
QY 61 TVTVNLIQRHGARWPTSGARQVAAVAKIQWARPFTDPKYEFLNDFYKKGVDLLPF 120
Db 61 TVTVNLIQRHGARWPTSGARQVAAVAKIQWARPFTDPKYEFLNDFYKKGVDLLPF 120
QY 121 GANQSHQTGDMTRYSTLFEQGVDPFVRAAGDQVRVDSSTNTWTAAGDASGETVLTQ 180
Db 121 GANQSHQTGDMTRYSTLFEQGVDPFVRAAGDQVRVDSSTNTWTAAGDASGETVLTQ 180
QY 181 VVLQEGNCTLCNNMCNEVDGDESTTLGVEFAPNITARLNAAAPSANLSDSALTMDM 240
Db 181 VVLQEGNCTLCNNMCNEVDGDESTTLGVEFAPNITARLNAAAPSANLSDSALTMDM 240
QY 241 CPFDTLSSGNASPFCDLFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVGYVNEILLARL 300
Db 241 CPFDTLSSGNASPFCDLFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVGYVNEILLARL 300
QY 301 TGOAVRDETQTNRTLDSDPATFPLNRTFYADPFSHNTMVPIFAALGLFNATLDPKPD 360
Db 301 TGOAVRDETQTNRTLDSDPATFPLNRTFYADPFSHNTMVPIFAALGLFNATLDPKPD 360
QY 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVQPLEFCGGVGVCELSAFVESQT 420
Db 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVQPLEFCGGVGVCELSAFVESQT 420
QY 421 YARENGQGDFAKCGFVPSE 439
Db 421 YARENGQGDFAKCGFVPSE 439

RESULT 3
US-08-989-358A-2
; Sequence 2, Application US/08989358A
; Patent No. 6060298
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren
; APPLICANT: Bech, Lisbeth
; APPLICANT: Fuglsang, Claus
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Ostergaard, Peter
; TITLE OF INVENTION: Peniophora Phytase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6060298 No. 6060298disk of No. 6060298th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,358A
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 1481/96
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; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: 0529/97
; FILING DATE: 07-MAY-1997
; APPLICATION NUMBER: 60/046,081
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5101.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-989-358A-2

Query Match 100.0%; Score 2325; DB 3; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAFAPSIILLSSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEG 60
DB 1 MVSSAFAPSIILLSSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEG 60
QY 61 TVTVQVNLIRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFYKFGVADLLPF 120
DB 61 TVTVQVNLIRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFYKFGVADLLPF 120
QY 121 GANQSHQGTQMDMYTRYSTLFEFGDVPFVRAAGDQRVVDSSTNWTAGFDGASGETVLTQL 180
DB 121 GANQSHQGTQMDMYTRYSTLFEFGDVPFVRAAGDQRVVDSSTNWTAGFDGASGETVLTQL 180
QY 181 VVLQEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAPSANLSDSALTMDM 240
DB 181 VVLQEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAPSANLSDSALTMDM 240
QY 241 CPEDTLSSGNASPCDLFTABEEVSVYDYLDKYYGTGPGNALGPVQGVYVNEILLARL 300
DB 241 CPEDTLSSGNASPCDLFTABEEVSVYDYLDKYYGTGPGNALGPVQGVYVNEILLARL 300
QY 301 TGOAVRDEQTNRITLSDPATFFLNRTFYADFSDHNTMVP1FAALGLFNATALDPLKPD 360
DB 301 TGOAVRDEQTNRITLSDPATFFLNRTFYADFSDHNTMVP1FAALGLFNATALDPLKPD 360
QY 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESAFVESQT 420
DB 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESAFVESQT 420
QY 421 YARENGQDPAKCGFVPE 439
DB 421 YARENGQDPAKCGFVPE 439
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RESULT 4

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US-09-273-871A-7
; Sequence 7, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
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; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Peniophora ycii
; US-09-273-871A-7
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Query Match 100.0%; Score 2325; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAFAPSIILLSSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEG 60
DB 1 MVSSAFAPSIILLSSSLALSTQFSFVAAQLPIPAQNTSNWGPYDPFFVPEYAAPPEG 60
QY 61 TVTVQVNLIRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFYKFGVADLLPF 120
DB 61 TVTVQVNLIRHGARWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDFYKFGVADLLPF 120
QY 121 GANQSHQGTQMDMYTRYSTLFEFGDVPFVRAAGDQRVVDSSTNWTAGFDGASGETVLTQL 180
DB 121 GANQSHQGTQMDMYTRYSTLFEFGDVPFVRAAGDQRVVDSSTNWTAGFDGASGETVLTQL 180
QY 181 VVLQEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAPSANLSDSALTMDM 240
DB 181 VVLQEGNCTLCNNMCPNEVDGDESTTWLGVFAPNITARLNAAPSANLSDSALTMDM 240
QY 241 CPEDTLSSGNASPCDLFTABEEVSVYDYLDKYYGTGPGNALGPVQGVYVNEILLARL 300
DB 241 CPEDTLSSGNASPCDLFTABEEVSVYDYLDKYYGTGPGNALGPVQGVYVNEILLARL 300
QY 301 TGOAVRDEQTNRITLSDPATFFLNRTFYADFSDHNTMVP1FAALGLFNATALDPLKPD 360
DB 301 TGOAVRDEQTNRITLSDPATFFLNRTFYADFSDHNTMVP1FAALGLFNATALDPLKPD 360
QY 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESAFVESQT 420
DB 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESAFVESQT 420
QY 421 YARENGQDPAKCGFVPE 439
DB 421 YARENGQDPAKCGFVPE 439
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RESULT 5

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US-09-482-558A-24
; Sequence 24, Application US/09482558A
; Patent No. 6569659
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens C.
; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/09/482,558A
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: US/08/993,359
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 1480/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 1481/96
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/ PRIOR FILING DATE: 1996-12-20
/ PRIOR APPLICATION NUMBER: 0301/97
/ PRIOR FILING DATE: 1997-03-18
/ PRIOR APPLICATION NUMBER: 0529/97
/ PRIOR FILING DATE: 1997-05-07
/ PRIOR APPLICATION NUMBER: 1388/97
/ PRIOR FILING DATE: 1997-12-01
/ PRIOR APPLICATION NUMBER: 60/046.082
/ PRIOR FILING DATE: 1997-05-09
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 24
/ LENGTH: 439
/ TYPE: PRT
/ ORGANISM: Peniophora lycii
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(30)
US-09-482-558A-24

Query Match      100.0%; Score 2325; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAFAPSIILLSSLSLALSTQFSFVAAQLPIPAQNTSNMGPDYDFFPVPYAAPPEGC 60
Db 1 MVSSAFAPSIILLSSLSLALSTQFSFVAAQLPIPAQNTSNMGPDYDFFPVPYAAPPEGC 60

QY 61 TVTVNLIQRHGAWPTSGARSRQVAQVAKIQMARPTDPKYEFLNDFYKFGVADLLPF 120
Db 61 TVTVNLIQRHGAWPTSGARSRQVAQVAKIQMARPTDPKYEFLNDFYKFGVADLLPF 120

QY 121 GANQSHQGTDMYRSTLFEQGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLTQ 180
Db 121 GANQSHQGTDMYRSTLFEQGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLTQ 180

QY 181 VVLQEGNCTLCNNCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM 240
Db 181 VVLQEGNCTLCNNCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM 240

QY 241 CPFDLTSSGNASPFCDLFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVVNEELLARL 300
Db 241 CPFDLTSSGNASPFCDLFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVVNEELLARL 300

QY 301 TQGAVRDETQTRNLDSDPATFPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPE 360
Db 301 TQGAVRDETQTRNLDSDPATFPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPE 360

QY 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQT 420
Db 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQT 420

QY 421 YARENGQGDFAKCGFVPS 439
Db 421 YARENGQGDFAKCGFVPS 439

RESULT 6
US-10-083-452-7
/ Sequence 7, Application US/10083452
/ Patent No. 6689358
/ GENERAL INFORMATION:
/ APPLICANT: Svendsen, Allan
/ TITLE OF INVENTION: Phytase Variants
/ FILE REFERENCE: 5618 500-US
/ CURRENT APPLICATION NUMBER: US/10/083,452
/ CURRENT FILING DATE: 2002-02-26
/ PRIOR APPLICATION NUMBER: US/09/273,871
/ PRIOR FILING DATE: 1999-03-22
/ PRIOR APPLICATION NUMBER: PA 1998 00407
/ PRIOR FILING DATE: 1998-03-23
/ PRIOR APPLICATION NUMBER: PA 1998 00806
/ PRIOR FILING DATE: 1998-06-19
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/ PRIOR APPLICATION NUMBER: PA 1998 01176
/ PRIOR FILING DATE: 1998-09-18
/ PRIOR APPLICATION NUMBER: PA 1999 00091
/ PRIOR FILING DATE: 1999-01-22
/ PRIOR APPLICATION NUMBER: 60/080,129
/ PRIOR FILING DATE: 1998-03-31
/ PRIOR APPLICATION NUMBER: 60/090,675
/ PRIOR FILING DATE: 1998-06-25
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 439
/ TYPE: PRT
/ ORGANISM: Peniophora ycii
US-10-083-452-7

Query Match      100.0%; Score 2325; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSSAFAPSIILLSSLSLALSTQFSFVAAQLPIPAQNTSNMGPDYDFFPVPYAAPPEGC 60
Db 1 MVSSAFAPSIILLSSLSLALSTQFSFVAAQLPIPAQNTSNMGPDYDFFPVPYAAPPEGC 60

QY 61 TVTVNLIQRHGAWPTSGARSRQVAQVAKIQMARPTDPKYEFLNDFYKFGVADLLPF 120
Db 61 TVTVNLIQRHGAWPTSGARSRQVAQVAKIQMARPTDPKYEFLNDFYKFGVADLLPF 120

QY 121 GANQSHQGTDMYRSTLFEQGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLTQ 180
Db 121 GANQSHQGTDMYRSTLFEQGDVPFVRAAGDQRVVDSSTNWTAGFGDASGETVLTQ 180

QY 181 VVLQEGNCTLCNNCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM 240
Db 181 VVLQEGNCTLCNNCPNEVDGDESTTWLGVFAPNITARLNAAAPSANLSDSALTMDM 240

QY 241 CPFDLTSSGNASPFCDLFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVVNEELLARL 300
Db 241 CPFDLTSSGNASPFCDLFTAEYVSVEYYDLDKYYGTGPGNALGPVQGVVNEELLARL 300

QY 301 TQGAVRDETQTRNLDSDPATFPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPE 360
Db 301 TQGAVRDETQTRNLDSDPATFPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPE 360

QY 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQT 420
Db 361 NRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAVQPLEFCGGVDGVCESLAFVESQT 420

QY 421 YARENGQGDFAKCGFVPS 439
Db 421 YARENGQGDFAKCGFVPS 439

RESULT 7
US-09-684-855-122
/ Sequence 122, Application US/09684855
/ Patent No. 6599735
/ GENERAL INFORMATION:
/ APPLICANT: F. Hoffmann-La Roche AG
/ TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
/ FILE REFERENCE: C38435/111692
/ CURRENT APPLICATION NUMBER: US/09/684,855
/ CURRENT FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: EP 00121663.9
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: EP 99120289.6
/ PRIOR FILING DATE: 1999-10-11
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 122
/ LENGTH: 419
/ TYPE: PRT
/ ORGANISM: P. lycii
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US-09-684-855-122

Query Match 96.3%; Score 2238; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.3e-240;
Matches 419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 STQSFVAAQLPIPAQNTSNWGPYDPPFVPEYAAAPPEGCTVTQVNLIOHGHARWPTSGA 80
DB 1 STQSFVAAQLPIPAQNTSNWGPYDPPFVPEYAAAPPEGCTVTQVNLIOHGHARWPTSGA 60
QY 81 RSRQVAAVAKIQWAPFTDPKYEFLNDVYKFGVADLLPFGANQSHQGTGDMYTRYSTLTF 140
DB 61 RSRQVAAVAKIQWAPFTDPKYEFLNDVYKFGVADLLPFGANQSHQGTGDMYTRYSTLTF 120
QY 141 EGGDVPFVRAAGQORVVDSTNTWTFAGDASGETVLPVLTQVVLQOEGNCTLCNNMCPNEV 200
DB 121 EGGDVPFVRAAGQORVVDSTNTWTFAGDASGETVLPVLTQVVLQOEGNCTLCNNMCPNEV 180
QY 201 DGDSESTTWLGVFAPNITARLNAAPSANLSDSALTMDMCPDFTLSSGNASPFCDLFTA 260
DB 181 DGDSESTTWLGVFAPNITARLNAAPSANLSDSALTMDMCPDFTLSSGNASPFCDLFTA 240
QY 261 EBYVSVEYYDLDKYYGTGPGNALGPVQGVYNNELLARLTGQAVRDETQTNRTLSDSPA 320
DB 241 EBYVSVEYYDLDKYYGTGPGNALGPVQGVYNNELLARLTGQAVRDETQTNRTLSDSPA 300
QY 321 TPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEK 380
DB 301 TPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEK 360
QY 381 LACSGKEARVRLVNDVAVQPLEFCGGVDGVCESAFVESQTYARENGQGFPAKCGFVPE 439
DB 361 LACSGKEARVRLVNDVAVQPLEFCGGVDGVCESAFVESQTYARENGQGFPAKCGFVPE 419

RESULT 8

US-09-488-265B-21
; Sequence 21, Application US/09488265B
; Patent No. 6720174
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; APPLICANT: Lassen, Soren F
; TITLE OF INVENTION: Improved Phytases
; FILE REFERENCE: 5808.200-US
; CURRENT APPLICATION NUMBER: US/09/488,265B
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Peniophora lycii
US-09-488-265B-21

Query Match 96.3%; Score 2238; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.3e-240;
Matches 419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 STQSFVAAQLPIPAQNTSNWGPYDPPFVPEYAAAPPEGCTVTQVNLIOHGHARWPTSGA 80
DB 1 STQSFVAAQLPIPAQNTSNWGPYDPPFVPEYAAAPPEGCTVTQVNLIOHGHARWPTSGA 60
QY 81 RSRQVAAVAKIQWAPFTDPKYEFLNDVYKFGVADLLPFGANQSHQGTGDMYTRYSTLTF 140
DB 61 RSRQVAAVAKIQWAPFTDPKYEFLNDVYKFGVADLLPFGANQSHQGTGDMYTRYSTLTF 120
QY 141 EGGDVPFVRAAGQORVVDSTNTWTFAGDASGETVLPVLTQVVLQOEGNCTLCNNMCPNEV 200
DB 121 EGGDVPFVRAAGQORVVDSTNTWTFAGDASGETVLPVLTQVVLQOEGNCTLCNNMCPNEV 180
QY 201 DGDSESTTWLGVFAPNITARLNAAPSANLSDSALTMDMCPDFTLSSGNASPFCDLFTA 260
DB 181 DGDSESTTWLGVFAPNITARLNAAPSANLSDSALTMDMCPDFTLSSGNASPFCDLFTA 240

QY 261 EBYVSVEYYDLDKYYGTGPGNALGPVQGVYNNELLARLTGQAVRDETQTNRTLSDSPA 320
DB 241 EBYVSVEYYDLDKYYGTGPGNALGPVQGVYNNELLARLTGQAVRDETQTNRTLSDSPA 300
QY 321 TPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEK 380
DB 301 TPLNRTFYADFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEK 360
QY 381 LACSGKEARVRLVNDVAVQPLEFCGGVDGVCESAFVESQTYARENGQGFPAKCGFVPE 439
DB 361 LACSGKEARVRLVNDVAVQPLEFCGGVDGVCESAFVESQTYARENGQGFPAKCGFVPE 419

RESULT 9

US-09-684-855-145
; Sequence 145, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 409
; TYPE: PRT
; ORGANISM: P. lycii
US-09-684-855-145

Query Match 94.2%; Score 2191; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 2.2e-235;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 LPIPAQNTSNWGPYDPPFVPEYAAAPPEGCTVTQVNLIOHGHARWPTSGARSRQVAQVAK 90
DB 1 LPIPAQNTSNWGPYDPPFVPEYAAAPPEGCTVTQVNLIOHGHARWPTSGARSRQVAQVAK 60
QY 91 IQWARPFTDPKYEFLNDVYKFGVADLLPFGANQSHQGTGDMYTRYSTLTFEGGDVFPVRA 150
DB 61 IQWARPFTDPKYEFLNDVYKFGVADLLPFGANQSHQGTGDMYTRYSTLTFEGGDVFPVRA 120
QY 151 AGDQRVVDSSTNTWTFAGDASGETVLPVLTQVVLQOEGNCTLCNNMCPNEVDGESTTWLG 210
DB 121 AGDQRVVDSSTNTWTFAGDASGETVLPVLTQVVLQOEGNCTLCNNMCPNEVDGESTTWLG 180
QY 211 VFAPNITARLNAAPSANLSDSALTMDMCPDFTLSSGNASPFCDLFTAEEYVSVEYY 270
DB 181 VFAPNITARLNAAPSANLSDSALTMDMCPDFTLSSGNASPFCDLFTAEEYVSVEYY 240
QY 271 DLDKYYGTGPGNALGPVQGVYNNELLARLTGQAVRDETQTNRTLSDSPAATPLNRTFYA 330
DB 241 DLDKYYGTGPGNALGPVQGVYNNELLARLTGQAVRDETQTNRTLSDSPAATPLNRTFYA 300
QY 331 DFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEKLACSGKEAVR 390
DB 301 DFSDHNTWVPIFAALGLFNATALDPLKPDENRLWVDSKLVPPFSGHMTVEKLACSGKEAVR 360
QY 391 VLVDVAVQPLEFCGGVDGVCESAFVESQTYARENGQGFPAKCGFVPE 439
DB 361 VLVDVAVQPLEFCGGVDGVCESAFVESQTYARENGQGFPAKCGFVPE 409

RESULT 10

US-09-684-855-137
; Sequence 137, Application US/09684855
; Patent No. 6599735

```
/ GENERAL INFORMATION:
/ APPLICANT: F. Hoffmann-La Roche AG
/ TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
/ FILE REFERENCE: C38435/111692
/ CURRENT APPLICATION NUMBER: US/09/684,855
/ CURRENT FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: EP 00121663.9
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: EP 99120289.6
/ PRIOR FILING DATE: 1999-10-11
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 137
/ LENGTH: 442
/ TYPE: PRT
/ ORGANISM: Basidio
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (1)..(442)
/ OTHER INFORMATION: n is unknown
/ NAME/KEY: UNSURE
/ LOCATION: (1)..(442)
/ OTHER INFORMATION: x is unknown
US-09-684-855-137

Query Match      57.9%; Score 1347; DB 4; Length 442;
Best Local Similarity 61.8%; Pred. No. 4e-141;
Matches 267; Conservative 32; Mismatches 111; Indels 22; Gaps 5;

QY 28 AAQLPPTAQTNSWGYDFFPVEPAAPPEGCTVQVNLQIHGARGWPTSGARSRQVAA 87
DB 9 AAQLPPIXQXQXWSYSPYFVAXYXAPPAGCQIXQVNIQRHGAREFTSGAATRIQAA 68
QY 88 VAKIQMARFPTDPKVEFLNDFVYKFGVADLLPFGANQSHQGTGDMVTRYSTLFEQGDVPE 147
DB 69 VAKLQSAAXXTDPKDLFLXNTYXGLGDDLVPFGAXQSQOAGQEAFTRYSLVSDNLPF 128
QY 148 VRAAGDQRVDSSTNWTAGFGDASGTBTVLPTQLVLEQEGNCTLCNNMCPNEVDG - EST 206
DB 129 VRASGSDRVDSATNWTAGFAXASXNTXXPKLVILSEXGNDTLDNMCXPAGDSDPQXN 188
QY 207 TWLGVFAPNITARLNAAPSAANLSDALTLMDCPPDTLSSGNASPFCDLP - TAEEVY 264
DB 189 XWLAVFAPITARLNAAPAGANLTDAXNLXLCPEFTVSEXXSXFCDLPEXXPEEFP 248
QY 265 SYEYYDLDKYGCTGPGNALGPVQGVYNELLARLTGOAVRDETQTNRTLSDPATPPL 324
DB 249 AFXYXGDLDFKFGTGGQPLGPVQGVYNELLARLTGOAVRDNQTQTNRTLSDSXPPL 308
QY 325 NRTFYADFSDHNTWVPPIFAALGLFNATA-LDPLKPDENRLWVDSKLVPPFSGHMTVEKLAC 383
DB 309 NRTFYADFSDHNTWVPPIFAALGLFNATA-LDPLKPDENRLWVDSKLVPPFSGHMTVEKLAC 368
QY 384 -----SKAEAVRLVNDVAPLEFCGG-VDGVCELSAFVESQTYAREN 425
DB 369 XXXGTXXXXXXXXXXXXXXXXVRLVNDVAPLEFCGGDXGXCXTLDADFVESQTYARE 428
QY 426 GQGDFAKCGFVP 437
DB 429 GQGDPEKCFATP 440

RESULT 11
US-08-993-359-26
/ Sequence 26, Application US/08993359A
/ Patent No. 6039942
/ GENERAL INFORMATION:
/ APPLICANT: Lassen, Soren F.
/ APPLICANT: Bech, Lisbeth
/ APPLICANT: Ohmann, Anders
/ APPLICANT: Breinholt, Jens
/ APPLICANT: Fugleang, Claus C.
/ APPLICANT: Ostergaard, Peter R.
```

```
/ TITLE OF INVENTION: Phytase Polypeptides
/ FILE REFERENCE: 5383.500-US
/ CURRENT APPLICATION NUMBER: US/08/993,359A
/ CURRENT FILING DATE: 1997-12-18
/ EARLIER APPLICATION NUMBER: 1480/96
/ EARLIER FILING DATE: 1996-12-20
/ EARLIER APPLICATION NUMBER: 1481/96
/ EARLIER FILING DATE: 1996-12-20
/ EARLIER APPLICATION NUMBER: 0301/97
/ EARLIER FILING DATE: 1997-03-18
/ EARLIER APPLICATION NUMBER: 0529/97
/ EARLIER FILING DATE: 1997-05-07
/ EARLIER APPLICATION NUMBER: 1388/97
/ EARLIER FILING DATE: 1997-12-01
/ EARLIER APPLICATION NUMBER: 60/046,082
/ EARLIER FILING DATE: 1997-05-09
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 26
/ LENGTH: 442
/ TYPE: PRT
/ ORGANISM: Paxillus involtus
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(19)
US-08-993-359-26

Query Match      51.8%; Score 1204; DB 3; Length 442;
Best Local Similarity 55.3%; Pred. No. 3.6e-125;
Matches 242; Conservative 51; Mismatches 139; Indels 6; Gaps 5;

QY 1 MVSSAFAPSIILSLMSSIALSTQFSFVAQAQLPIPAQNTSNMGPDPFFVEPEYAAAPGEC 60
DB 1 MLFGFVALACLLSLSEVLATSVPKN-TAFTPIPESEQRNWSPSYPFLAEYKAPPACG 59
QY 61 TVTQVNLQIHGARGWPTSGARSRQVAAVAKIQMARPFTDPKYEFLNDPVYKFGVADLLPF 120
DB 60 QINQVNIQRHGAREFTSGATTRIKAGLTKLQGVQNFDAKFNFKSEKYDLGNSDLVPF 119
QY 121 GANQSHQGTGDMVTRYSTLFEQGDVPEFVRAAGDQRVDSSTNWTAGFGDASGETVLP 180
DB 120 GAAQSFDAQEAFAFYKLVKXNNLFFTRADGSDRVDSATNWTAGFASASINTVQPKLN 179
QY 181 VVLQEGNCTLCNNMCPNEVDG - ESTTWLGVFAPNITARLNAAPSAANLSDALTLM 239
DB 180 LILPQTGNDTLEDNMCRAAGSDPQVNAWLAFAFPSITARLNAAPSVNLTDTDAFNLS 239
QY 240 MCPFTLSSGNASPFCDLFTA--EYVSEYIYDLDKYGTGPGNALGPVQGVYNELL 297
DB 240 LCAFLTVSEKKSDPCTLFEIGIPGSEFAFAYGGDLDFKFTGYGQELGPVQGVYNELI 299
QY 298 ARLTGOAVRDETQTNRTLSDPATPPLNRTFYADFSDHNTWVPPIFAALGLFNATA-LDPL 356
DB 300 ARLTNSAVRDNQTQTNRTLSDPATPPLNKTIFYADFSDHNLWVAFSAMGLFRQAPLSTS 359
QY 357 KPDENRLWVDSKLVPPFSGHMTVEKLACSGKEAVRVLVNDVAPLEFCGG-VDGVCELSAF 415
DB 360 VNPWRTRWTSLSLVFSGRMVVERLSCFGTTKVRVLVDQVQVPLEFCGDRNGLCTLAKF 419
QY 416 VESQTYARENGOGDPAC 433
DB 420 VESQTFARSDGAGDFEC 437

RESULT 12
US-09-482-558A-26
/ Sequence 26, Application US/09482558A
/ Patent No. 6569659
/ GENERAL INFORMATION:
/ APPLICANT: Lassen, Soren F.
/ APPLICANT: Bech, Lisbeth
/ APPLICANT: Ohmann, Anders
/ APPLICANT: Breinholt, Jens
```

APPLICANT: Fugleang, Claus C.
APPLICANT: Ostergaard, Peter R.
TITLE OF INVENTION: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
CURRENT APPLICATION NUMBER: US/09/482,558A
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: US/08/993,359
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 1480/96
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 1481/96
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 0301/97
PRIOR FILING DATE: 1997-03-18
PRIOR APPLICATION NUMBER: 0529/97
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 1388/97
PRIOR FILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: 60/046,082
PRIOR FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 442
TYPE: PRT
ORGANISM: Paxillus involutus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-09-482-558A-26

Query Match 51.8%; Score 1204; DB 4; Length 442;
Best Local Similarity 55.3%; Pred. No. 3.6e-125;
Matches 242; Conservative 51; Mismatches 139; Indels 6; Gaps 5;
QY 1 MYSSAFAPISLLSLSSALSTQSFVAAQLPPTPAQNTSNWGYDPPFPVYAAPEGC 60
DB 1 MFGFVALACLSSLVLTSPKN-TAPTFPIPESEQRNWSYSPFLAEYKAPAGC 59
QY 61 TVTVQNLIQRHGARWPTSGARSQVAAVAKIQMARPTDPKYEFLNDVYKFGVADLLPF 120
DB 60 QINQVNIQRHGARWPTSGATTIKAGLTKLQGVQNTDAKFNFIKSFYDLGNSDLVFF 119
QY 121 GANQSHQTGDMTRYSTLFEQGVDPFVRAAGDQVRVDSSTNWTAGFGDASGETVLTQ 180
DB 120 GAAQSPDAGQEAARYSKLVKNLFFIRADGSDRVVDSATNWTAGFASASHNTVQPKLN 179
QY 181 VVLOEGNCTLCNNMCPNEVDGD-ESTTWLGVPAPNITARLNAAAPSANLSDALTMD 239
DB 180 LILPQTGNDTLEONMCPAAGSDPQVNAVLAVFPSTITARLNAAAPSVNLTDADFNLVS 239
QY 240 MCPFDTLSSGNASPPCDLFTA--EYVSVYDYDLDKYYGTGEGNALGPVQGVYVNELL 297
DB 240 LCAFLTVSEKKSDFCTLFEGIPGSFEAFAYGGDLKFKYGTGQBELGPVQGVYVNELI 299
QY 298 ARLTQAVRDETQTNRTLSDPATFPLNRTFYADFSDHNTWMPPIPAALGLFNATA-LDPL 356
DB 300 ARLTNSAVRDNQTQTNRTLDASPTVTFPLNKTMYADFSDHNLWAVFSAMGLFRQAPPLSTS 359
QY 357 KPDENLWDSKLVPFSGHMTVEKLACSGKEARVLVNDVAVQVLEFCGG-VDGVCFLSAP 415
DB 360 VNPFWRTWTSLLVPFSGRMVVERLSCFGTKRVRLVQVQVQVLEFCGGDRNGLCTLAKP 419
QY 416 VESQTYARENGQGDFAKC 433
DB 420 VESQTFARSDGAGDFEKC 437

RESULT 13
US-08-993-359-28
; Sequence 28, Application US/08993359A
; Patent No. 6039942
; GENERAL INFORMATION:

APPLICANT: Lassen, Soren F.
APPLICANT: Bech, Lisbeth
APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Fugleang, Claus C.
APPLICANT: Ostergaard, Peter R.
TITLE OF INVENTION: Phytase Polypeptides
FILE REFERENCE: 5383.500-US
CURRENT APPLICATION NUMBER: US/08/993,359A
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 1480/96
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 1481/96
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 0301/97
PRIOR FILING DATE: 1997-03-18
PRIOR APPLICATION NUMBER: 0529/97
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 1388/97
PRIOR FILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: 60/046,082
PRIOR FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 442
TYPE: PRT
ORGANISM: Paxillus involutus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-08-993-359-28

Query Match 51.7%; Score 1202; DB 3; Length 442;
Best Local Similarity 52.6%; Pred. No. 6e-125;
Matches 230; Conservative 61; Mismatches 128; Indels 18; Gaps 5;
QY 2 VSSAFAPISLLSLSSALSTQSFVAAQLPPTPAQNTSNWGYDPPFPVYAAPEGC 61
DB 14 LSEVFAASVPRN-----IAPKFSIPSEQRNWSYSPFLAEYKAPAGCE 60
QY 62 TVTVQNLIQRHGARWPTSGARSQVAAVAKIQMARPTDPKYEFLNDVYKFGVADLLPF 121
DB 61 INQVNIQRHGARWPTSGATTIKAGLTKLQGVQNTDPKFDIKSFYDLGTSDLVFP 120
QY 122 ANQSHQTGDMTRYSTLFEQGVDPFVRAAGDQVRVDSSTNWTAGFGDASGETVLTQ 181
DB 121 AAQSPDAGLEVPARYSKLVSSDNLPFIRSDGSDRVVDTATNWTAGFASARNAIQPKLDL 180
QY 182 VVLOEGNCTLCNNMCPNEVDGD-ESTTWLGVPAPNITARLNAAAPSANLSDALTMD 240
DB 181 ILPQTGNDTLEONMCPAAGSDPQVNAVLAVFPSTITARLNAAAPGANLTDADFNLVSL 240
QY 241 CPFDTLSSGNASPPCDLFTA--EYVSVYDYDLDKYYGTGEGNALGPVQGVYVNELLA 298
DB 241 CEFMTVSEKKSDFCTLFEGIPGSFEAFAYAGDLKFKYGTGQALGPVQGVYVNELLA 300
QY 299 RLTVQAVRDETQTNRTLSDPATFPLNRTFYADFSDHNTWMPPIFAALGLFNATA-LDPL 357
DB 301 RLTVNSAVRDNQTQTNRTLDAAPTFPLNKTMYADFSDHNLWAVFSAMGLFRQAPPLSTS 360
QY 358 KPDENLWDSKLVPFSGHMTVEKLACSGKEARVLVNDVAVQVLEFCGG-VDGVCFLSAP 416
DB 361 PDENRTWTSLLVPFSGRMVVERLSCAGTKRVRLVQVQVQVLEFCGGDQGLCALDKFV 420
QY 417 ESQTYARENGQGDFAKC 433
DB 421 ESQAYARSDGAGDFEKC 437

RESULT 14
US-09-273-871A-4
; Sequence 4, Application US/09273871A

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; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involutus
; US-09-273-871A-4
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Query Match 51.7%; Score 1202; DB 4; Length 442;
Best Local Similarity 52.6%; Pred. No. 6e-125;
Matches 230; Conservative 61; Mismatches 128; Indels 18; Gaps 5;
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QY 2 VSAFAPSILLMSLSLSTOFSFVAAQLPTPAQNTSNWGYDPFPFVPEYAAPEGCT 61
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
14 LSEVFAASVPRN-----IAPKFSIPESQQRNWSYSPYFPLAEYKAPGACG 60

QY 62 VTQVNLIIQRHGAWPTSGARSQVAIAKIOWARPTDPKYEFNDVYKFGVADLLPFG 121
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 INQVNLIIQRHGAWPTSGAATRIKAGLSKQSVQNFDPKDFIKSFYDYDLGTSDLVPPG 120

QY 122 ANQSHQTGTDTRYSTLTFEGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPQLQV 181
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 AAQSPDAGLEVFAFYSLVSSDNLPIRSDGSDRVVDATNTWTAGFASARNAIQPKLDL 180

QY 182 VLQEGNCTLCNNMCPNEVDGD-ESTTWLGVPAPNITARLNAAAPSANLSDSALTLMDM 240
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 ILPQTGNDTLEDNMCPAAGESDPQVDWLASAPPSVTAQLNAAAPGANLTDADAFNLVSL 240

QY 241 CPFDTLSSGNASPPCDLFTA--EEYVSVEYYVDLDKYYGTGPGNALGPVQGVYNELLA 298
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
299 RLITGOAVRDETQTNRTLSDPATFPLNRTFYADFSDHNTMVPFIAPALGLFNATA-LDPLK 357
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 RLITNSAVNDTQTNRTLDAAPDTFPLNKTMYADFSDHNLVAVFSAMGLFRQSAPLSTST 360

QY 358 PDENRLWDSKLVPSGHTMVKLACSGKEARVRLVNDVAVQPLEFCGG-VDGVCSELSAFV 416
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 PDENRLWDSKLVPSGHTMVKLACSGKEARVRLVNDVAVQPLEFCGG-VDGVCSELSAFV 416

QY 417 ESQTVARENGQGDFAKC 433
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 ESQAVARSGGAGDFEKC 437
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```
RESULT 15
US-09-482-558A-28
; Sequence 28, Application US/09482558A
; Patent No. 6569659
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
```

```
; APPLICANT: Fugleang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/09/482,558A
; CURRENT FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: US/08/993,359
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 1480/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 1481/96
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 0301/97
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: 0529/97
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 1388/97
; PRIOR FILING DATE: 1997-12-01
; PRIOR APPLICATION NUMBER: 60/046,082
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Paxillus involtus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)....(19)
; US-09-482-558A-28
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Query Match 51.7%; Score 1202; DB 4; Length 442;
Best Local Similarity 52.6%; Pred. No. 6e-125;
Matches 230; Conservative 61; Mismatches 128; Indels 18; Gaps 5;
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QY 2 VSAFAPSILLMSLSLSTOFSFVAAQLPTPAQNTSNWGYDPFPFVPEYAAPEGCT 61
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
14 LSEVFAASVPRN-----IAPKFSIPESQQRNWSYSPYFPLAEYKAPGACG 60

QY 62 VTQVNLIIQRHGAWPTSGARSQVAIAKIOWARPTDPKYEFNDVYKFGVADLLPFG 121
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 INQVNLIIQRHGAWPTSGAATRIKAGLSKQSVQNFDPKDFIKSFYDYDLGTSDLVPPG 120

QY 122 ANQSHQTGTDTRYSTLTFEGDVPFVRAAGDQVRVDSSTNWTAGFGDASGETVLPQLQV 181
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 AAQSPDAGLEVFAFYSLVSSDNLPIRSDGSDRVVDATNTWTAGFASARNAIQPKLDL 180

QY 182 VLQEGNCTLCNNMCPNEVDGD-ESTTWLGVPAPNITARLNAAAPSANLSDSALTLMDM 240
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 ILPQTGNDTLEDNMCPAAGESDPQVDWLASAPPSVTAQLNAAAPGANLTDADAFNLVSL 240

QY 241 CPFDTLSSGNASPPCDLFTA--EEYVSVEYYVDLDKYYGTGPGNALGPVQGVYNELLA 298
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
299 RLITGOAVRDETQTNRTLSDPATFPLNRTFYADFSDHNTMVPFIAPALGLFNATA-LDPLK 357
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 RLITNSAVNDTQTNRTLDAAPDTFPLNKTMYADFSDHNLVAVFSAMGLFRQSAPLSTST 360

QY 358 PDENRLWDSKLVPSGHTMVKLACSGKEARVRLVNDVAVQPLEFCGG-VDGVCSELSAFV 416
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 PDENRLWDSKLVPSGHTMVKLACSGKEARVRLVNDVAVQPLEFCGG-VDGVCSELSAFV 416

QY 417 ESQTVARENGQGDFAKC 433
Db : |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 ESQAVARSGGAGDFEKC 437
```

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Search completed: May 27, 2005, 08:34:00
Job time : 45 secs
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